OM protein

Run on:

Sequence:

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CC344833 960 bp DNA linear GSS 16-MAY-2003 OGIAQ20TV ZM 0.7 1.5 KB Zea mays genomic clone ZMMBMa0359C15, genomic survey sequence.
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BCC053418 G
BMO9840 C
CC0865620 M
CC028437 3
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CC719566
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Tel: 301-838-5845
Fax: 301-838-0208
Email: whitelaw@tigr.org
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TIGR
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LOCUS
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                              GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Jatabase

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Minimum DB Maximum DB

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Arabidops Arabidops

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HVSMEc001 OGYCI 27TH HI15H04r EST737031

1007056A0

Arabidope

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EBes01 SQ CGF100422 Mddb5012p 3591 1 10 HVSMEKÖ01

EBes01_SQ OGWIF61TV 1123005E0

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methylation filtered genomic DNA library"
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DNA linear GSS 22-AUG-2003
genomic clone ZMMBMa0788E05,
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methylation filtered genomic DNA library"
                                                                                                                                                                                                                                       9712 Medical Center Drive, Rockville, MD 20850,
Tel: 301-838-5843
Fax: 301-838-0208
Email: whitelaw@tigr.org
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Matches:
Conservative:
Mismatches:
Indels:
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1. 923
Argan="Zea mays"
/mol type="genomic DNA"
/gtrain="B73"
CCTCATACGCAGCCTTTGGGTCCTTCT 884
                                               923 bp
Zea mays
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                                                      Genomic survey sequence. CG240397.1 GI:34140283 GSS.
                                              CG240397
OGYCI27TV ZM_0.7_1.5_KB
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96.21%
95.52%
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Class: sheared ends
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CC344824 B73 bp DNA linear GSS 16-MAY-2003 OGIAQ20TH ZM 0.7_1.5_KB Zea mays genomic clone ZMMBMa0359C15, genomic survey sequence.
CC344824
GC344824.1 GI:30814230
GSS.
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1 (basea 1 to 818)
Whitelaw,C.A., Quackenbush,J., Van Aken,S., Utterback,T., Resnick,A., Fraser,C.M., Budiman,M.A., Bedell,J.A., Rohlfing,T., Consortium for Maize Genomics
Consortium for Maize Genomics
Other GSSs: OGSAA40TH
Contact: Cathy Whitelaw
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1. 818
/organiam="Zea mays"
/mol type="genomic DNA"
/strain="B73"
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Zea mays c
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9712 Medical Center Drive, Rc
Tel: 301-838-5843
Fax: 301-838-0208
Email: whitelaw@tigr.org
Seq primer: TF
Class: sheared ends.
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CG9AD40TV ZM_0.7_1.5_KB Ze
genomic survey sequence.
CG451578
CG451578.1 GI:34838578
GSS.
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867 bp DNA linear GSS 23-JUN-2003 GGLAB23TV ZM 0.7 1.5 KB Zea mays genomic clone ZMMBMa0307C22, genomic survey sequence. CC724960 CC724960.1 GI:32143893 GSS.
                                                                  251
                                                                                    GTCGCAGCAGGCGGAGATGGGGGGTGACGGTGAAGCTGGTGGACTTTGCCCATGTG 273
                                                                                                                                    271
                                                                                                                                                     Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD calde; Panicoideae; Andropogoneae; Zea.

1 (Bases 1 to 867)
Whitelaw, C.A., Guackenbush, J., Van Aken, S., Utterback, T., Citek, R.W., Nunberg, A., Robbins, D. and Lakey, N. Consortium for Maize Genomics
Other GSSs: OGLAB2TH
Contact: Cathy Whitelaw
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                 392 GAGCAGACTCTGTTCCACTCTACTCGGCGTCGATTCTTCTGGGCTATGATGCTGCAC
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 GluGlnThrLeuPheHisPheTyrSerAlaSerIleLeuLeuGlyTyrAspAlaAla
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methylation filtered genomic DNA library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9712 Medical Center Drive, Rockville, MD 20850,
Tel: 301-838-5843
Fax: 301-838-0208
Email: whitelaw@tigr.org
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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Class: sheared ends.
Location/Qualifiers
1.867
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JOURNAL
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AUTHORS
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CC724960
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                            Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnollophyta; Liliopsida, Poales, Poaceae, PACCAD Cade; Panicoideae, Andropogoneae, Zea.

(bases 1 to 873)
Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T., Resnick, A., Fraser, C.M., Budiman, M.A., Bedell, J.A., Rohlfing, T., Citek, R.W., Nunberg, A., Robbins, D. and Lakey, N.
Consortium for Maize Genomics
Unpublished (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 812 ACGCGACTCCTCCCCACCGAGGCGCAGCCCGGGGGAGCCGCATCCTCACCTCGTCCTCGAC 753
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/clone="zwhBMa0359015"
/clone_lib="zM_0.7 1.5_KB"
/note="vector: pBGSK-; Site_1: HincII; 0.7-1.5 kb
methylation filtered genomic DNA library"
                                                                                                                                                                                                                     9712 Medical Center Drive, Rockville, MD 20850, USA Tel: 301-838-5643 Fax: 301-838-0208 Email: whitelaw@tigr.org
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Matches:
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Mismatches:
Indels:
Gaps:
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/mol type="genomic DNA"
/strain="B73"
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Location/Qualifiers
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JOURNAL
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Fax: 301-838-0208
Email: whitelaw@tigr.org
Seq primer: TR
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Location/Qualifiers
1. 719
/ organia="Zea mays"
/ mol type="genomic DNA"
/ ferrain="B73"
/ db xxef="teaxon:4577"
/ clone="ZWBMa0584K02"
/ clone=lib="ZM-2M-07 1:5-KB"
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1 (bases 1 to 719)
Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T., Resnick, A., Fraser, C.M., Budiman, M.A., Bedell, J.A., Rohlfing, T., Citek, R., Nunberg, A., Robbins, D. and Lakey, N.
Consortium for Maize Genomics
Unpublished (2002)
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301-838-5843
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Contact: Cathy Whitelaw
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The libraries that made SUCEST
Genet. Mol. Biol. 24 (1-4), 1-7 (2001)
Contact: Arruda P
Contro de Biologia Molecular e Engenharia Genetica
Universidade Estadual de Campinas
Caixa Postal 6010, 13083-970, Campinas SP, Brazil
Tel: 55 19 3788 1137
Fax: 55 19 3788 1089
Email: parruda@unicamp.br
Clone distribution: clone distribution information can be found through the Brazilian Clone Collection Center (BCCC) at http://www.bcccenter.fcav.unesp.br
                                                                         ProGlyGluProHisProHisLeuValLeuAspAspLeuLeuAlaGlyPheGlnAlaPro 100
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//alone "Organ: Root tips (0.3cm-long) from adult plants;
//alone "Organ: Root tips (0.3cm-long) from adult plants]. Sitel, An unidirectional CDNA library generated from [Root tips (0.3cm-long) from adult plants]. CDNA was prepared from polysh mRNA using Superscript Plasmid System Kit (Invircedn). The double-strand cDNAs were fractionated in a sepharose CL-2B 40cm-columns and fragments sizing between 0.8 and 1.5 Kb were directionally cloned into the vector. Details of each source of RNA and library construction can be obtained at http://sucest.lad.ic.unicamp.br/public"
                                                                                         SCJFRT1061H11.g RT1 Saccharum officinarum cDNA clone SCJFRT1061H11 CA134480
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
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Clone distribution: clone distribution information can be found
through the Brazilian Clone Collection Center (BCCC) at
http://www.bcccenter.fcav.unesp.br
Plate: 061 row: H column: 11
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Vetrore, A.L., da Silva, F.R., Kemper, B.L. and Arruda, P. The libraries that made SUCEST Genet. Mol. Biol. 24 (1-4), 1-7 (2001)
Genet. Mol. Biol. 24 (1-4), 1-7 (2001)
Contact: Arruda P
Contact: Arruda P
Contror de Biologia Molecular e Engenharia Genetica
Universidade Estadual de Campinas
Caixa Postal 6010, 13083-970, Campinas SP, Brazil
Fel: 55 19 3788 1039
Fex: 55 19 3788 1089
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/mol_type="mRNA"
/mol_type="mRNA"
/clore="SCJFRT1061H11"
/lab_hogt="DH10B"
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/dloine libe "RIT"
/cloine libe 
                                                                                                                                                                                                                                                                                                                  Saccharum officinarum
Saccharum officinarum
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta;
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACCAD
clade, Panicoideae, Andropogoneae, Saccharum, Saccharum officinarum
                                                                                                                          CALJUGBS 722 bp MRNA linear EST 24-SEP-2003 SCCCRT1004G05.g RT1 Saccharum officinarum cDNA clone SCCCRT1004G05 5', mRNA sequence.
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Clone distribution: clone distribution information can be found
through the Brazilian Clone Collection Center (BCCC) at
http://www.bcccenter.fcav.unesp.br
Plate: 004 row: G column: 05
Seq primer: T7 Promoter Primer.
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Contact: Arruda P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Centro de Biologia Molecular e Engenharia Genetica
Universidade Estadual de Campinas
Caixa Postel 6010, 13083-970, Campinas SP, Brazil
TEI: 55 19 3788 1137
Fax: 55 19 3788 1089
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Matches:
Conservative:
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/clone="SCCCRT1004G05"
/lab_host="DH10B"
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200 uSerGinLeuArgGluLeuLys 207
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                         633 GTCACAGCTGCGCGAGCTTAAG
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CA130685.1 GI:35013914
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VERSION
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                                                                                                                                                                                                        /ub host="DH10B"
/lab host="DH10B"
/clone lib="Saccharum officinarum FL5"
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Matches:
Conservative:
Mismatches:
Indels:
                                                                                                       /organism="Saccharum officinarum"
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                                                                                                                                   /mol_type="mRNA"
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/clone="SCBGFL5081A03"
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                      Seg primer: T7 Promoter Primer.
Location/Qualifiers
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/dev_stage="adult"
/lab_host="DH103" - RescueMu Grid L"
/clone_lib="1123 - RescueMu Grid L"
/note="Organ : leaf; Vector: RescueMu (engineered from pBlueScript backbone); Site 1: BamH1; Site 2: BglII;
RescueMu is a 4.9 kb, modified maize Mu transposon designed to allow plasmid rescue from total genomic DNA. Wu elements insert preferentially into transcription units. For more information on RescueMu, go to the web site 'www.rmdb.iastate-edu' and follow the links for 'RescueMu. Grid L was grown in Molokai in 2001. DNA was extracted from leaf strips, double digested using BamHI and BglII, and ligated to form circular plasmids. DH10B cells were transformed and then screened on LB plates with ampicillin."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CA202412 671 bp mRNA linear EST 25-SEP-2003 SCRLFL1009H02.g FL1 Saccharum officinarum cDNA clone SCRLFL1009H02 5', mRNA sequence.
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Mukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopaida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 591)
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Unpublished (2001)
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                              CCAGGGGAGCCGCATCCGCACCTCGTCCTCGACGACCTCCTCGCGGGGCTGGAGGCCCCC
                                                                                                                                                                                                                            TGCGTCGCCGACATCAAGATCGGCGCCATCACGTGGCCGCCGCGCCGAGCTCGCCGGAGCCCTAC
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                                                                                                                                          ProGlyGluProHisProHisLeuValLeuAspAspLeuLeuAlaGlyPheGlnAlaPro
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           GlyGluHisGluValAlaPheTyrGluAlaPheSerAlaHisAlaAlaValProAlaArg
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/tissue_type="leaf"
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Stanford University
B55 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
Email: walbotostenford.edu
Plate: 1123005
Class: transposon-tagged.
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/organism="Zea mays"
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601

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Direct Submission
Submitted (25-ARR-2002) Maize Mapping Project, University of Missouri, Columbia, MO 65211, USA
Missouri, Columbia, MO 65211, USA
If you are interested in getting corresponding physical clones, these are publicly available from ZmDB and may be found by BLAST searching at MSL, maizemap.org; ZmDB, www.ramb.iastate.edu, TIGR, www.tigr.org; or NCBI, www.ncbi.nlm.nih.gov. When the source of the maize CDNA sequences is either Virginia Walbot, Stanford or Pat Schnable, Iowa State, then clones may be requested from ZmDB: www.zmdb.iastate.edu.
Location/Qualifiers
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
Clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 3374)
Hainey,C.F., Dolan, M., Morgante,M., Whitsitt,M.S.,
Arthur,L.W., Hanafey,M., Morgante,M. and Tingey,S.V.
Maize Mapping Project/DuPont Consensus Sequences for Design of
Overgo Probes
2 (bases 1 to 3374)
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                                                                                                                                                                                                                                                                                                                                                                                                 161 LysAlaMetAspThrAlaGlyValArgArgValLeuArgArgTyrValSerSerValAla
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                                           141 SerGlyValArgValValGlyProGluGlyAlaValTrpArgThrGluArgProGluVal
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/db_xref="taxon:4577"
/clone_lib="Maize Mapping Project/DuPont Cornsensus
Library"
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//lab host="DHIOB"
//lab host="DHIOB"
//lab host="Organ: Inflorescence at begining of development
//note="Organ: Inflorescence at begining of development (Icm-long); Vector: pSport1; Site 1: Sal1; Site 2: Not1;
An unidirectional cDNA library generated from
[Inflorescence at begining of development (Icm-long)].
CDNA was prepared from polyA+ mRNA using SuperScript
Plasmid System Kit (Invitrogen). The double-strand cDNAs
were fractionated in a sepharose CL-28 40cm-columns and
fragments sizing between 0, 8 and 1.5 KD were
directionally cloned into the vector. Details of each
source of RNA and library construction can be obtained at
                                                                     Saccharum officinarum
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Lillopsida, Poales, Poaceae, PACCAD
clade, Panicoideae, Andropogoneae, Saccharum, Saccharum officinarum
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Centro de Biologia Molecular e Engenharia Genetica
Universidade Estadual de Campinas
Caixa Postal 6010, 13083-970, Campinas SP, Brazil
Tel: 55 19 3788 1189
Email: 55 19 3788 1089
Email: parrudaçunicamp.br
Clone distribution: clone distribution information can be found through the Brazilian Clone Collection Center (BCCC) at http://www.bcccenter.fcav.unesp.br
http://www.bcccenter.fcav.unesp.br
Plate: 009 row: H column: 02
Seq primer: TY Pronocer Primer.
Location/Qualifiers
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The libraries that made SUCEST
Genet. Mol. Biol. 24 (1-4), 1-7 (2001)
Contact: Arruda P
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722 bp DNA linear GSS 23-JUN-2003 GOLAB23TH ZM_0.7_1.5_KB Zea mays genomic clone ZMMBMa0307C22, genomic survey sequence.
CC724950.1 GI:32143883
                                                                                                   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD calde; Panicoideae; Andropogoneae; Zea.

1 (Dases 1 to 72)
Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T., Citek, R.W., Nunberg, A., Robbins, D. and Lakey, N. Consortium for Maize Genomics
Other GSSs: OGIAB23TV
Contact: Cathy Whitelaw
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/clone lib="zw 0.7 1.5 KB"
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                                       Length:
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Mapping Project"
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FGASO23256 Triticum aestivum FGAS: Library 6 CAP GATE 1 Triticum aestivum cDNA, mRNA sequence.
CK211413
CK211413.1 GI:39617517
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Triticum aestivum (bread wheat)
Triticum aestivum (bread wheat)
Triticum aestivum (bread wheat)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
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//clone libe All libe RRI.
//clone libe All libe RRI.
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CA130686.1 GI:35013916
EST.
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Clone distribution: clone distribution information can be found
clone distribution: clone distribution information can
chrough the Brazilian Clone Collection Center (BCCC) at
http://www.bccenter.fcav.uneap.br
Plate: 004 row: G column: 06
Seg primer: T7 Promoter Primer.
Location/Qualifiers
                            PCybalaLeualaalaalaValTyrGlyGlyLyBGlyGlyValLeuSerGlnLeuArgGl
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Vettore, A.L., da Silva, F.R., Kemper, E.L. and Arruda, P. The libraries that made SUCEST
Genet. Mol. Biol. 24 (1-4), 1-7 (2001)
Contact: Arruda P
Centro de Biologia Molecular e Engenharia Genetica
Universidade Estadual de Campinas
Caixa Postal (610, 13083-970, Campinas SP, Brazil
Tel: 55 19 3788 1089
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          and Arruda, P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Saccharum officinarum
Saccharum officinarum
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CA130686
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/dD xere="Feaxon:4565"
/dDome lib=Taxon:4565"
/clone lib=Taxion:4565"
/note="Organ: Crown and leaf; Vector: pCMV.SPORT6; Crown
(50%) and leaf (50%) tissues from wheat cultivar Norstar
after short exposure times to low temperature in the light
and in the dark. 12 mRNA populations were combined before
constructing the library. The first 6 populations: After 7
days of growth at 2002 from wheat cultivar Norstar after
short exposure times to low temperature in the light and
in the dark. 12 mRNA populations were combined before
constructing the library. The first 6 populations: After 7
days of growth at 20, wheat plants were transferred to 4C
in the light. 1cm crown sections and green leaf tissu were
separature exposure. The last 6 populations: After 7
days of growth at 20C, wheat plants were transferred to 4C in
the dark. 1cm crown sections and green leaf tissu were
separature exposure. The last 6 populations: After 7
days
of growth at 20C, wheat plants were transferred to 4C in
the dark. 1cm crown sections and green leaf tissu were
separately harvested after 1, 3, and 6 hours of low
temperature exposure. First strand synthesis in this
library was done in the presence of methylated dCTP
thereby protecting from internal cleaved with NotI. In
addition, this library used a primer for second strand
synthesis that annealed to an artificial sequence (ANA)
                                                                                                                                                                                                                                                                                                                                                                                                         University of Saskatchewan, Department of Computer Science
1C101 Engineering Building, 57 Campus Drive, Saskatoon,
Saskatchewan, S7N 5A9, Canada
1Tel: 306 966 2033
Email: figas estsecs.usask.ca
Email: figas estsecs.usask.ca
This sequence is the direct result of the Base calling software
This sequence is the direct result of the Base calling the
identification of the high quality insert the software Lucy
(default parameters) has been run on this sequence. Lucy identified
the region [1,797].
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Pooldeae, Triticeae, Triticum.
1 (bases 1 to 1191)
1 (alare, F., Crosby, W.L., Danyluk, J., Eudes, F., Frick, M., Gaudet, D., Genswein, B., Graf, R., Gullck, P., Hrycan, L.D., Laroche, A., Links, M.G., McCarthy, R.L., Monroy, A., Muzak, I., Nilson, D., Penniket, C., Roach, J.L. and Sarhan, F.
Functional Genomics of Abiotic Stress In Wheat and Canola Crops
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                                                                                                                                                                                                                                                                                      Unpublished (2003)
Contact: Wm L Crosby
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                                      REFERENCE
AUTHORS
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JOURNAL
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US-10-042-894A-8 (1-289) x CK211413 (1-1191)

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944 677 677 888 824 824 1107 704 1147 1185 127 127 127 127 127 127 127 127 127 127	TTTAACACGGCCTTTTCCGCCC	ProargPheHisGlyThrargl	HisbeuvalLeuAspAspleul :::									GlyLeuCysSerLeulleLysE
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Search completed: June 17, 2005, 06:34:53 Job time : 3703 secs

²⁷ GlySerGlyLeuPheTyrLysProLeuGlnAlaGlyAspArgGlyGluHisGluValAla 46

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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OM protein - nucleic search, using frame plus p2n model
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June 17, 2005, 05:35:00 ; Search time 2130 Seconds (without alignments) 842.244 Million cell updates/sec	US-10-042-894A-8 1521 1 MSDLHPPEHQVAGHRASASKIKFVSDIVPETPHTQPLGPS 289	BLOSUM62 Xgapop 10.0 , Xgapext 0.5 Ygapop 10.0 , Ygapext 0.5 Fgapop 6.0 , Fgapext 7.0 Delop 6.0 , Delext 7.0
June	US-1 1521 1 MS	Xgal Ygal Ygal Fgal
Run on:	Title: Perfect score: Sequence:	Scoring table:

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Listing first 45 summaries

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ALIGNMENTS

RESULT 1			
US-10-042-894A-7			
: Seguence 7, Application US/10042894A			
; Publication No. US20030009011A1			
; GENERAL INFORMATION:			
; APPLICANT: Shi, Jinrui			
; APPLICANT: Beach, Larry			
; APPLICANT: Wang, Hongyu			
; APPLICANT: Rafalski, Antoni J.			
; APPLICANT: Cahoon, Rebecca E.			
; TITLE OF INVENTION: No. US20030009011A1el Inositol Polyphosphate Kinas	Inositol	Polyphosphate	Kina
TITLE OF INVENTION: Genee and Uses Thereof	ų		
; FILE REFERENCE: 1286			
; CURRENT APPLICATION NUMBER: US/10/042,894A			
; CURRENT FILING DATE: 2002-01-09			
POTOR APPLICATION NUMBER: US 60/261.465			

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                                                                                                               JUNEAU PRICATION NO. US2003009011A1

Sequence 5, Application US/10042894A

Publication No. US20030009011A1

GENERAL INFORMATION:

APPLICANT: Shi, Jinrui

APPLICANT: Beach, Larry

APPLICANT: Rafalski, Antoni J.

TITLE OF INVENTION: No. US20030009011A1e1 Inositol Polyphosphate Kinan

TITLE OF INVENTION: Genes and Uses Thereof

TITLE OF INVENTION: Genes and Uses Thereof

CURRENT APPLICATION NUMBER: US/01/042,894A

CURRENT PLING DATE: 2001-01-09

PRIOR FILING DATE: 2001-01-12

NUMBER OF SEQ ID NOS: 37

SOTWARRE FASESEQ for Windows Version 4.0

SEQ ID NO 5

LENGTH: 203

TYPE: DNA

ORCANISM: Zea mays

FRATURE:

NAME/KEY: CDS

LOCATION: (33)...(922)

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Matches:
Conservative:
Mismatches:
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PRIOR FILING DATE: 2001-01-12
NUMBER OF SEQ ID NOS: 37
SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 7
                                                                                                                                4.71e-172
1521.00
100.00%
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Best Local Similarity:
Query Match:
DB:
                                          LENGTH: 1344
TYPE: DNA
ORGANISM: Zea mays
                                                                                  ; NAME/KEY: CDS
; LOCATION: (52)
US-10-042-894A-7
                                                                                                                   Alignment Scores:
Pred. No .
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Squance 3, Application US/10042894A

Squance 3, Application US/10042894A

Publication No. US20030009011A1

GENERAL INFORMATION:

APPLICANT: Bach, Larry

APPLICANT: Rafalski, Antoni J.

APPLICANT: Rafalski, Antoni J.

APPLICANT: Rafalski, Antoni J.

TITLE OF INVENTION: No. US20030009011A1el Inositol Polyphosphate Kinase

TITLE OF INVENTION: Genes and Uses Thereof

FILE REFERENCE: 1286

CURRENT APPLICATION NUMBER: US/10/042,894A

CURRENT FILING DATE: 2002-01-09

PRIOR APPLICATION NUMBER: US 60/261,465

PRIOR PILICA DATE: 2001-01-12

NUMBER OF SEQ ID NOS: 37

SOFTWARE: FastSEQ for Windows Version 4.0
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US-10-425-115-74438

US-10-425-115-74438

Sequence 74438, Application US/10425115

Publication No. US20040214272A1

GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21 (53222)B
CURRENT FILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 369326

SEQ ID NO 74438

LENGTH: 1426
                                                                                                                                                                                                                                                                                                                                         ABRPHeLeuGlyGlyLeuCysSerLeuIleLysPheValSerAspIleValProGluThr 280
                                                                              LysAlaMetAspThrAlaGlyValArgArgValLeuArgArgTyrValSerSerValAla 180
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                                                                                              AspGluGlyMetAspCysAlaLeuAlaAlaAlaValTyrGlyGlyGlyGlyValLeu
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    ATCGCCAAGTGCCTCGCCATGGACCGCGGGACCACGAGGGTTCTGCTCGGATTCCGCGTC
                           SerGlyValArgValValGlyProGluGlyAlaValTrpArgThrGluArgProGluVal
                                                      GACGAGGGGATGGACTGTGCGCTGCGGGGGGTGTACGGAGGAAAAGGTGGAGTTTG
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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ORGANISM: Zea mays
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APPLICANT: Shi, Jinrui

APPLICANT: Shi, Jinrui

APPLICANT: Beach, Larry

APPLICANT: Beach, Larry

APPLICANT: Rafalski, Antoni J.

APPLICANT: Rafalski, Antoni J.

APPLICANT: Cahoon, Rebecca E.

ITILE OF INVENTION: No. US2003009911A1e1 Inositol Polyphosphate Kinase

ITILE OF INVENTION: Genes and Uses Thereof

FILE REFERENCE: 1286

CURRENT FILING DATE: 2002-01-09

PRIOR PALICATION NUMBER: US 60/261,465

PRIOR FILING DATE: 2001-01-12

NUMBER OF SEQ ID NOS: 37

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 1

LENGTH: 1169
   833 CAACTICCTGGGGGGGCTCTGCTAGCTGATCAAGTTCGTTTCTGACATTGTTCCAGAGAC 892
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         141 SerGlyValArgValValGlyProGluGlyAlaValTrpArgThrGluArgProGluVal 160
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                           rProHisThrGlnProLeuGlyProSer
                                         US-10-042-894A-1; Sequence 1, Application US/10042894A; Publication No. US20030009011A1; GENERAL INFORMATION:
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; CRGANISM: Zea mays
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (84)...(80
US-10-042-894A-1
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Query Match:
DB:
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                                                                                                                         Length:
Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                               US-10-042-894A-8 (1-289) x US-10-042-894A-3 (1-923)
                                                                                                                                                                                         Gaps:
                                                                                                                         5.97e-162
1435.00
96.21%
95.52%
94.35%
                                                                         ... (736)
                                                                                                                                                 Percent Similarity:
Best Local Similarity:
                         TYPE: DNA
ORGANISM: Zea mays
                                                           ; NAME/KEY: CDS
; LOCATION: (53)
US-10-042-894A-3
                                                                                                              Alignment Scores
SEQ ID NO 3
LENGTH: 923
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                                                  FEATURE:
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DB:
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Sequence 15, Application US/10042894A
; Sequence 15, Application US/10042894A
; Publication No. US2030009011A1
; GENERAL INFORMATION:
; APPLICANT: Shi, Jinrui
; APPLICANT: Beach, Larry
; APPLICANT: Rafalski, Antoni J.
; TITLE OF INVENTION: No. US2030009011A1e1 Inositol Polyphosphate Kinase
; TITLE OF INVENTION: Genes and Uses Thereof
; TITLE OF INVENTION: Genes and Uses Thereof
; FILE REFERENCE: 1286
; CURRENT APPLICATION NUMBER: US/10/042,894A
; CURRENT FILING DATE: 2002-01-09
; PRIOR FILING DATE: 2001-01-12
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121 IleAlaLysCysLeuAlaLysAspArgGlyThrThrSerValLeuLeuGlyPheArgVal
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; Sequence 20, Application US/20030009011A1
; General INFORMATION:
    APPLICANT:
    AP
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     TTGC--GTCCGAGTCGTCGGCCCCGGAGGCCCCTGTGGCGGAGCGGAGCGCCCGGAGGTG
                                                        LysAlaMetAspThrAlaGlyValArgArgValLeuArgArgTyrValSerSer-ValAl
                                                                             aAspGluGlyMetAspCysAlaLeuAlaAlaAlaValTyrGlyGlyLyGlyValLe
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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1307.00
90.34$
89.66$
85.93$
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Best Local Similarity:
Query Match:
DB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA
ORGANISM: Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; NAME/KEY: CDS
; LOCATION: (72)
US-10-042-894A-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 6
US-10-042-894A-20
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Sequence 4650, Application US/10437963
; Sequence 4650, Application US/10437963
; Publication No. US2004012334341
; Publication No. US2004012334341
; APPLICANT: A cos Thomas J.
; APPLICANT: Cao, Yongwei
; APPLICANT: Cao, Yongwei
; APPLICANT: Cao, Yongwei
; APPLICANT: Barbazuk, Brad
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; TITLE OF INVENTION: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; ROWNER OF SEQ ID NOS: 204966
; TENNER OF SEQ ID NOS: 204966
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CysValAlaAspileLysIleGlyAlaileThrTrpProProSerSerProGluProTyr 120
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                        ; OTHER INFORMATION: Clone ID: PAT_MRT4530_11514C.1
US-10-437-963-4650
                                                                                                                                                                                                                                                                                                                                                                                                  1.76e-127
1148.50
84.45%
77.03%
                                              280 rProHisThrGln 284
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                                                                                                                                                                                                                                                                                                                        TYPE: DNA
ORGANISM: Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                                     Percent Similarity:
Best Local Similarity:
Query Match:
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Pred. No.:
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                                                                                                                                  899
248
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                                                                                                                                  Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                            US-10-042-894A-8 (1-289) x US-10-042-894A-15 (1-899)
             4.0
             Version
NUMBER OF SEQ ID NOS: 37
SOFTWARE: FastSEQ for Windows
SEQ ID NO 15
LENGTH: 899
                                                                                                                                  9.8e-138
1233.00
88.42%
87.02%
81.07%
                                                                           ; NAME/KEY: CDS
; LOCATION: (89)...(424)
US-10-042-894A-15
                                                                                                                                                       Percent Similarity:
Best Local Similarity:
Query Match:
DB:
                                            TYPE: DNA
ORGANISM: Zea mays
FEATURE:
                                                                                                                        Alignment Scores:
Pred. No.:
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Sequence 17, Application US/10042894A

Publication No. US20030009011A1

GENERAL INROMATION:

APPLICANT: Shi, Jinrui

APPLICANT: Beach, Larry

APPLICANT: Reacleki, Antoni J.

APPLICANT: Rafalski, Antoni J.

APPLICANT: Rafalski, Antoni J.

APPLICANT: Cahoon, Rebecca E.

TITLE OF INVENTION: No. US20030009011A1e1 Inositol Polyphosphate Kinase

TITLE OF INVENTION: Genes and Uses Thereof

TITLE OF INVENTION: US/10/042,894A

CURRENT APPLICATION NUMBER: US/10/042,894A

CURRENT FILING DATE: 2001-01-12

PRIOR FILING DATE: 2001-01-12
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                  62 ArgAspThrPhePheProArgPheHisGlyThrArgLeuLeuProThrGluAlaGlnPro
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APPLICANT: La Rosa, Thomas J.
APPLICANT: Sovalic, David K.
APPLICANT: Sov, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Boukharov, Andrey A.
APPLICANT: Burbazuk, Brad
APPLICANT: Li, Ping
APPLICANT: Ping
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    SerGlyvalArgvalvalGlyProGlu---GlyAlavalTrpArgThrGluArgProGlu
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Matches:
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ORGANISM: Oryza sativa
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ORGANISM: Parthenium argentatum FEATURE:
  PRIOR APPLICATION NUMBER: US 60,
PRIOR FILING DATE: 2001-01-12
NUMBER OF SEQ ID NOS: 37
SOFTWARE: FastSEQ for Windows V6;
SEQ ID NO 13
LENGTH: 1020
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742.50
67.83%
52.10%
48.82%
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Best Local Similarity:
                                                                                                   ; NAME/KEY: CDS
; LOCATION: (21)
US-10-042-894A-13
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Pred. No.:
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Publication No. US2003009011A1
Publication No. US2003009011A1
Publication No. US2003009011A1
APPLICANT: Seach, Larry
APPLICANT: Mang, Hongyu
APPLICANT: Mang, Hongyu
APPLICANT: Refalski, Antoni J.
APPLICANT: Cahoon, Rebecca E.
TITLE OF INVENTION: No. US20030009011A1e1 Inositol Polyphosphate Kinase
FILE REFERENCE: 1286
CURRENT APPLICATION NUMBER: US/10/042,894A
CURRENT FILING DATE: 2002-01-09
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                                                                            NAME/KEY: misc feature
LOCATION: (1)...(643)
OTHER INFORMATION: n = A, T, C
NUMBER OF SEQ ID NOS: 37
SOFTWARE: FastSEQ for Windows
SEQ ID NO 17
LENGTH: 643
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808.50
93.14%
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Percent Similarity:
Best Local Similarity:
Query Match:
DB:
                                              TYPE: DNA
ORGANISM: Zea mays
FEATURE:
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US-10-042-894A-13
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Matches:
Conservative:
Mismatches:
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Version
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143 Valargvalval -- - GlyProGluGlyAlaValTrpArgThrGluArgProGluValLy9 161
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530 CTAAGGGTATATCAAATAGCGAAGCTGGATTITGGCAACCTGAGAAGAAGGTTGTTAT
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LOCATION: (12)...(851)
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Sequence 11, Application VS2003009011A1

GENERAL INFORMATION:
APPLICANT: Shi, Jinrui
APPLICANT: Shi, Jinrui
APPLICANT: Refalski, Antoni J.
APPLICANT: Wang, Hongyu
APPLICANT: Gahoon, Rebecca E.
TITLE OF INVENTION: No. US20030009011A1el Inositol Polyphosphate Kinase
TITLE OF INVENTION: Genes and Uses Thereof
TITLE OF INVENTION: WO. US20030009011A1el Inositol Polyphosphate Kinase
CURRENT APPLICATION NUMBER: US/10/042,894A
CURRENT FILING DATE: 2002-01-09
PRIOR PILING DATE: 2001-01-12
NUMBER OF SEQ ID NOS: 37

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 11
LENGTH: 1195
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                                                          851
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    GGTGCT----CGGTCAAACGCAGAAGTCAAACTTATTGATTTTGCTCATGTTACAGATGGT 791
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                              255 AspGlyVal11eAspHisAsnPheLeuGlyGlyLeuCysSerLeuIleLysPheValSer
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Matches:
Conservative:
Mismatches:
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852 GACATACTTTCGGAGACA 869
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52.84$
47.50$
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ORGANISM: Eucalyptus grandis
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; LOCATION: (116)...(1048)
US-10-042-894A-11
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Best Local Similarity:
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APPLICANT: Shi, Jinrui
APPLICANT: Shi, Jinrui
APPLICANT: Beach, Larry
APPLICANT: Beach, Larry
APPLICANT: Rafalski, Antoni J.
APPLICANT: Rafalski, Antoni J.
APPLICANT: Rafalski, Antoni J.
APPLICANT: Cahoon, Rebecca E.
TITLE OF INVENTION: No. US20030009011A1el Inositol Polyphosphate Kinase
TITLE OF INVENTION: Momes and Uses Thereof
FILE REFERENCE: 1286
CURRENT APPLICATION NUMBER: US/10/042,894A
CURRENT FILING DATE: 2002-01-09
PRIOR APPLICATION NUMBER: US 60/261,465
PRIOR FILING DATE: 2001-01-12
NUMBER OF SEQ ID NOS: 37
SOFTWARE: FastSEQ for Windows Version 4.0
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Matches:
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                                                                                                  Length:
Matches:
Conservative:
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                             ; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_67156C.1
US-10-424-599-106467
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62.72%
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Query Match:
DB:
  TYPE: DNA
ORGANISM: Glycine
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Publication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Expu Yihua
APPLICANT: Cao Vongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53223)
ECURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 106467
LENGTH: 1345
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|TISTAG------GACTCTATCTCCTCCTGGGAACCTACCAGGAATCTCTCCAGTGT 485
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            163 MetAspThrAlaGlyvalArgArgValLeuArgArgTyrvalSerSer------
ProGluHisGlnValAlaGlyHisArgAlaSerAlaSerLysLeuGlyProLeuIleAsp
                                                                                                                                                                       63 AspThrPhePheProArgPheHisGlyThrArgLeuLeuProThrGluAlaGlnProGly
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US-10-424-599-106467
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US-10-425-115-74436
; Sequence 7436, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Labou, Yihua
; APPLICANT: CAO., Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; TITLE OF INVENTION: Plants
; FITLE OF INVENTION: UNBER: US/10/425,115
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 74436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                252 AlaGluGlyAapGlyValIleAapHisAanPheLeuGlyGlyLeuCysSerLeuIleLya 271
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Matches:
Conservative:
Mismatches:
Indels:
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; OTHER INFORMATION: Clone ID: MRT4577_167884C.1
US-10-425-115-74436
                                                                                                                                                                                                                                                NAME/KEY: unsure
LOCATION: (1)..(776)
OTHER INFORMATION: unsure at all n locations
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Percent Similarity:
Best Local Similarity:
Query Match:
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ORGANISM: Zea mays
FEATURE:
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Sequence 6, Appli Sequence 6, Appli Sequence 13, Appli Sequence 13, Appli Sequence 13, Appli Sequence 27, Appli Sequence 27, Appli Sequence 1213, Appli Sequence 1208, Appli Sequence 1208, Appli Sequence 1265, Appli Sequence 1265, Appli Sequence 1255, Appli Sequence 1255, Appli Sequence 1259, Appli Sequence 1654, Appli Sequence 1654, Appli Sequence 1653, Appli

Sequence 914, App Sequence 1091, Ap Sequence 1218, Ap Sequence 2, Appli

FOR THE DETECTION OF BLOOD CELL GENE

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COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: Ploppy disk
COMPUTER: Ploppy disk
COMPUTER: Ploppy disk
COMPUTER: PLOPS MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/023,655
FILING DATE: HEREWITH
CLASSIFICATION:
PRIOR APPLICATION DATA:
FILING DATE:
FILING DATE:
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FILING DATE:
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                                                                                                          US-09-902-540-1091
US-09-902-540-1218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 809, Application US/09023655; Patent No. 6607879; GENERAL INFORMATION: Application US/09023655; Patent No. 6607879; GENERAL INFORMATION: Application G. Stuart APPLICANT: Cocke, Benjamin G. APPLICANT: Jeffrey J. Seilhamer TITLE OF INVENTION: COMPOSITION FOR THE DE: TITLE OF INVENTION: EXPRESSION NUMBER OF SEQUENCES: 1508
CORRESPONDENCE ADDRESSE: ADDRESSES: ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-103-840A-2
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REGISTATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA-0001 US
TELECOMMUNICATION INFORMATION:
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   Command line parameters:
-MODEL=frame+ p2n.model -DEV=xlh
-Q=CQG12_1VGFO_EQPDO_IVG10042894/runat 15062005_111951_8314/app_query.fasta_1.455
-Q=CQG12_1VGFO_EQPO_IVG10042894/runat 15062005_111951_8314/app_query.fasta_1.455
-QG12_1VGFO_EQPD_IVG1042894/runat END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
-LIST45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
-USER=US10042894_@CGN_1 1_69_@runat_15062005_111951_8314 -NCPU=6 -ICPU=3
-NO MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
                                                                                                                                                                                                       June 17, 2005, 03:46:13; Search time 205 Seconds (without alignments) 2306.751 Million cell updates/sec
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2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/1/ina/ptorys COMB.seq:*
6: /cgn2_6/ptodata/1/ina/ptorys COMB.seq:*
                                  GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                     OM protein - nucleic search, using frame_plus_p2n model
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US-09-949-016-4634
US-09-248-796A-5436
US-09-248-796A-5436
US-09-949-016-2348
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US-09-248-796A-4664
US-09-248-796A-4664
US-09-252-991A-12872
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Maximum Match 100%
Listing first 45 summaries
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Xgapop 10.0, Ygapext (Ygapop 10.0, Ygapext (Ygapop 6.0, Fgapext Delop 6.0, Delext
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Maximum DB seq length: 200000000
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Perfect score:
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821 TGGTCATTTATGATGGCAAGGAGCGGCCCGAAGTGGTCCTGGACTCAGATGCTGAGGATT 880
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CURRENT FILING DATE: 2000-07-19
PRIOR APPLICATION NUMBER: 09/552,317
PRIOR FILING DATE: 2000-04-25
PRIOR FILING DATE: 2000-01-21
NUMBER OF SEQ ID NOS: 1105
SEQ ID NO 712
                                                                                                                                                                                                                                                                                       Sequence 712, Application US/09620312D Patent No. 6569662
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1.04e-11
189.00
45.27%
29.22%
                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: Tang, Y. Tom
APPLICANT: Liu, Chenghua
APPLICANT: Asundi, Vinod
APPLICANT: Asundi, Vinod
APPLICANT: Chen, Feiyan
APPLICANT: Chen, Rui-hong
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Percent Similarity:
Best Local Similarity:
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US-09-620-312D-712
                                                                                                                                                                                                                                                                              US-09-620-312D-712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURE:
NAME/KEY: CDS
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Pred. No.:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   124 ysLeuAlalysAspArgGlyThrThrSerValLeuLeuGlyPheArgValSerGlyValA 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 rgValValGlyProGluGlyAlaValTrpArgThrGluArgProGluValLysAlaMetA 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    605 AGGTGTAC-----CAAGCAGCAG-TGGGCAGCTCATGTTCATGAACA-AGTACCATGG 656
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            204 rgGluLeuLysAlaTrpPheGluGluGlnThrLeuPheHisPheTyrSerAlaSerIleL 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ----- 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           338 CCCAGCTTAAACACTATAACCCTTGGAGCATGAAATGTCACCAGCAACAGTTACAGAGAA 397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  398 T------GAAGGAGAATGCAAAGCATCGGAACC 424
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                                                                                                                                                                                                                                                                                                                                    GluHisGlnValAlaGlyHisArgAlaSerAlaSerLys-LeuGlyProLeuIleAspGl
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Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                         US-10-042-894A-8 (1-289) x US-09-023-655-809 (1-1341)
                                                                                                                                                                                                                                                                                                                                                                                               27 ySerGlyLeuPheTyrLysPro-------
                                                                                                                                                                                                          ength:
            TELEPAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: 809:
SEQUENCE CHARACTERISTICS:
LENGTH: 1341 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: BRAITUT01
CLONE: 753522
   (650) 855-0555
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40.36%
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12.69%
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Best Local Similarity:
Query Match:
    TELEPHONE:
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1001 ATGGCGAGGACACCGTGGTGCATGAGGCCCAG-----GATGCTGGCTATATCTTCG 1051
                                         881 TGGAGGACCTGTCAGAGGAATCAGCTGATGAGTCTGCTGGTGCCTATGCCTACAAACCCA 940
                                                                                                                                                                     -----ValAlaGluGlyAspGlyValIleAspHisAsnPheLeuGlyG 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                237 --AspGlyGlyValThrValLysLeuValAspPheAlaHis------
                                                                                                                                                                                                                                                                                265 lyLeuCysSerLeulleLysPheValSerAspileValProGluThr 280
---AlaAlaAlaValAlaAlaGlyGly-
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APPLICANT: Wang, Jian-Rui
APPLICANT: Zhou, Ping
APPLICANT: Wang, Yunging
APPLICANT: Wang, Zhiwei
APPLICANT: Wang, Zhiwei
APPLICANT: Wang, Zhiwei
APPLICANT: Drmanac, Radoje T.
APPLICANT: Drmanac, Radoje T.
TITLE OF INVENTION: NO. 6569662el Nucleic Acids and
TITLE OF INVENTION: Polypeptides
FILE REFERENCE: 784CIP2B
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Matches:
Conservative:
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474 CATACCACATACAAGGGCTACTGGAATGAGCACACCACCTACGATGGACCA---GACCCT 1530
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                                                                                                                                                                                                                                                                                                                                                                 ArgAspThrPhePhePro------ArgPheHisGlyThrArgLeuLeu 75
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NUMBER OF SEQ ID NOS: 441
SOFTWARE: pt_Ft_genes Version 2.0
SEQ ID NO 103
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26.17%
11.97%
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                                                                        TYPE: DNA ORGANISM: Homo sapiens
                                                                                                                                                                                                                               Percent Similarity:
Best Local Similarity:
Query Match:
DB:
                                                                                                                     ; NAME/KEY: CDS
; LOCATION: (367)
US-09-774-528-103
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Pred. No.:
                                                        LENGTH: 1863
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                                                                                                                                                      137 yPheArgValSerGlyValArgValValGlyProGluGlyAlaValTrpArgThrGluAr 157
                        eGlnAlaProCysValAlaAspIleLysIleGlyAlaIleThrTrpProProSerSerPr
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APPLICANT: Liu, Chenghua
APPLICANT: Asundi, Vinod
APPLICANT: Asundi, Vinod
APPLICANT: Asundi, Vinod
APPLICANT: Zhang, Jie
APPLICANT: Zhang, Jie
APPLICANT: Chenghua
APPLICANT: Wehrman, Tom
APPLICANT: Wehrman, Tom
APPLICANT: Wenny, Jian-Rul
APPLICANT: Wang, Jian-Rul
APPLICANT: Wang, Dunrul
APPLICANT: Dramanac, Radoje T.
TITLE OF INVENTION: Polypeptides
TITLE OF INVENTION: Polypeptides
TITLE OF INVENTION: Polypeptides
TITLE OF INVENTION: Polypeptides
CURRENT PLING DATE: 2001-01-30
                                                                                                                                                                                                                                                                                                                                                                                                              217 sPheTyrSerAlaSerIleLeuLeuGlyTyrAsp------
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; Sequence 103, Application US/09774528
; Patent No. 6743619
; GENERAL INFORMATION:
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Zhou, Ping
Goodrich, Ryle
Liu, Chenghua
Asundi, Vinod
Ren, Feiyan
Zhang, Jie
Zhao, Qing A.
Yang, Yonghong
Xue, Aidong J.
Wehrman, Tom
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JUNE OF THING DATE: 2000-10-30

PRIOR APPLICATION NUMBER: US/9949016

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REFERENCE: CL001307

CURRENT FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR PELICATION NUMBER: 60/241,756

PRIOR FILING DATE: 2000-10-20

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-09-08

PRIOR FILING DATE: 2000-09-08

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTHARE: FREESE FREESE (FW WINDOWS VERSION 4.0)

SEQ ID NO 4634

LENGTH: 1781
                 90 LeuAspAspLeuLeuAlaGlyPheGlnAlaProCysValAlaAspIleLySIleGlyAla 109
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                                                                ------AlaAlaAlaValAlaAlaGlyGlyAspGlyGlyGlyValThr
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Matches:
Conservative:
Mismatches:
Indels:
AlaSerIleLeuLeuGlyTyrAsp
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Best Local Similarity:
Query Match:
DB:
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; ORGANISM: Human
US-09-949-016-4634
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Pred. No.:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            148 ProGluGlyAlaValTrpArgThrGluArgProGluValLysAlaMetAspThrAlaGly 167
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TITLE OF INVENTION: No. 6743619e1 Nucleic Acids and
TITLE OF INVENTION: Polypeptides
FILE REFERENCE: 802
CURRENT APPLICATION NUMBER: US/09/774,528
CURRENT FILING DATE: 2001-01-30
NUMBER OF SEQ ID NOS: 441
SOFTWARE: PL FL genes Version 2.0
SEQ ID NO 102
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Mismatches:
Indels:
Gaps:
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Matches:
                               Sequence 102, Application US/09774528
Patent No. 6743619
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178.50
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                                                                              Tang, Y. Tom
Zhou, Ping
Goddrich, Ping
Liu, Chenghua
Asundi, Vinod
Ren, Feiyan
Zhao, Qing A.
Yang, Yonghong
Xue, Aidong J.
Wehrman, Tom
Wang, Jian-Rui
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Best Local Similarity:
Query Match:
DB:
                                                                GENERAL INFORMATION:
APPLICANT: Tang, Y
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: CDS
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ed. No.: 2.59e-06 Matches: 39.00 Matches: 67 conservative: 48 Et Local Similarity: 9.14* Mismatches: 10.642-894A-8 (1-289) x US-09-248-796A-5436 (1-963) 2 SerAspLeuHisproProGluHisGlnValAlaGlyHisArgAlaSerAlaSer 2 SarAspCeuHisproProGluHisGlnValAlaGlyHisArgAlaSerAlaSer 2 SarAspCeuHisproProGluHisGlnValAlaGlyHisArgAlaSerAlaSer 2 SarAspCeuHisproAAAAACAAAGAGGGGAGGACATATTCTCATATCA	Oy 20 LysLeuGlyProLeulleAspOlySerGlyLeupheiyllysparoLeucin 36	1	117 ProgluProTyrIleAlaLysCysLeuAlaLysAspArgGlyThrThrSerValLeuLeu 117 ProgluProTyrIleAlaLysCysLeuAlaLysAspArgGlyThrThrSerValLeuLeu 1187 ACTATCACCAAACAATCACATCGAGCTAAAAGCCAGAAGCACAACAAGAAAATTG 137 GlyPheArgValSerGlyValArgValValGlyProGluGlyAlaValTrpArgThrGlu	547 ĠĠTGTTÄĠÀATATGGĠÄCTTCAAATCTTTAATATCAAAACAAATTTTCTATCAGGAT 157 ArgProGluValLysAlaMetAspThrAlaGlyValargArgValLeuArgArgTyrVal 157 ArgProGluValLysAlaMetAspThrAlaGlyValArgArgValLeuArgArgTyrVal 157 ArgProGluValLysAlaMetAspCysAlaLeuAlaAlaAlaValTyrGlyGlyLys 177 SerSerValAlaAspGluGlyMetAspCysAlaLeuAlaAlaAlaValTyrGlyGlyLys 15::	Qy 197 Gly
Db 752 CTGCAGGACCTGCTCGATGGCTTCGACGGACCTTGTGTGTTCGACTGCAAAATGGGCGTC 811 Qy 110 IleThrTrp	136 LeuGlyPheArgValSerGlyValArgValValGlyProGluGlyAlaValTrpArg	Cy 170 ArgValLeuArgArgArgTyrValSerSerValAlaAspGlUGlYMetAspCysAlaLeuAla 189 Db 1112 GAAGTGCTGAGGCGGTAT	Db 1160 CTGCAGGTATCCGAGTTCTTCAGGAGGCCACGAGGTGATCGGCAGCTCCTTTTGTG 1219 Qy 227 TYTABDAlaAlaAlaAlaAlaAlaGlyGlyABpGlyGlyGlyGlyAlTrValLyBLeuVal 246 1220 CACGATCACTGCCATCGCGCCCGCGTGTGGCTCATC 1255 CV 247 ARDPHABLAHIAVALALAGINGLYARDGIVVAITIBARDHIA		SULT 6 Sequence 5436, Application US/09248796A Sequence 5436, Application US/09248796A Sequence 5436, Application US/09248796A PARENT NO. 6747137 APPLICANT: Keith Weinstock et al TITLE OF INVENTION: WOULEIC ACID AND AMINO ACID SEQUENCES RELATING TO TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS FILE REFERENCE: 107196.132 CURRENT APPLICATION NUMBER: US/09/248,796A FILE REPLICATION NUMBER: US 60/094,725 PRIOR APPLICATION NUMBER: US 60/096,409 PRIOR APPLICATION NUMBER: US 60/096,409 SEQ ID NOS: 28208 SEQ ID NOS: 28208 TYPE: DNA ORGANISM: Candida albicans -09-248-796A-5436 ignment Scores:

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APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REFERENCE: CLOOL1307

CURRENT APPLICATION NUMBER: US/09/949,016

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR FILING DATE: 2000-10-20

PRIOR PELING DATE: 2000-10-3

PRIOR FILING DATE: 2000-10-3

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

SOFTWARS: FactSEQ for Windows Version 4.0

SEQ ID NOS: 207012

SOFTWARS: PACTSEQ for Windows Version 4.0
      174 rgTyrValSerSerValAlaAspGluGlyMetAspCysAlaLeuAla-----AlaAlaV 192
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                                                                                                 864 AGGTACCAGCTCTTGCAACCGCCCACGCTCCAGACGCTGCGGTCCAGCTTGCGTTGGAGG
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ORGANISM: Human
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US-09-949-016-2348
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RESULT 7

US-09-252-991A-6525/c

Sequence 6525, Application US/09252991A

Sequence 6525, Application US/09252991A

Sequence 6521795

GENERAL INFORMATION:
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS;
TITLE OF INVENTION: APERCHINGS FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: NUMBER: US/09/252,991A

CURRENT APPLICATION NUMBER: US/09/252,991A

CURRENT FILING DATE: 1999-02-18

PRIOR FILING DATE: 1999-02-18

PRIOR FILING DATE: 1998-02-18

PRIOR FILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142
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Mismatches:
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Matches:
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:359 TGGATCGACTTTGGGAAAACCACGCCCTGCCTGAGGGCCCAGACCTTGCAGGATGAT 1418
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Matches:
Conservative:
Mismatches:
Indels:
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PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
SOFTWARE: PSEC ID NOS: 207012
SOFTWARE: PSECSE FOR Windows Version 4.0
TENGTH: 4505
TYPE: DNA
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Query Match:
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US-09-949-016-323
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Patent No. 6812339
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: VIOLANCE Et al.
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
TILE REFERENCE: CLO1307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
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| GRANGATGGGAATCAGGACCTACCTGGAGGAGCTCACGAAGGCCCGGAAGAAGCCC
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                       PhePheProArgPheHisGlyThrArgLeuLeuProThrGluAlaGlnProGlyGluPro
                                                                                                         HisProHisLeuValLeuAspAspLeuLeuAlaGlyPheGlnAlaProCysValAlaAsp
                                                                                                                                                  852 TACAACCAG-----ATGGACGACCTGCTGGCCGACTTCGACTCGCCCTGTGTGATGGAC
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GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: Keith Weinstock et al

APPLICANT: Keith Weinstock et al

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICANS

TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS

FILE REPERENCE: 107196.132

CURRENT APPLICATION NUMBER: US/09/248, 796A

CURRENT APPLICATION NUMBER: US 60/074, 725

PRIOR FILING DATE: 1998-02-13

PRIOR FILING DATE: 1998-08-13

NUMBER OF SEQ ID NOS: 28208

SEQ ID NO 4664
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                                                                                                                                                                                                                                                                                                                                                                        g---ArgvalleuArgArgTyrvalSerServalAlaAspGluGlyMetAspCys---- 186
                                   114 oSerSerProGluProTyrIleAlaLysCysLeuAlaLysAspArgGlyThrThrSerVa 134
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                                                                                     2449 Grececergecacergergeegacecececececes
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Matches:
Conservative:
Mismatches:
Indels:
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Best Local Similarity:
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Patent No. 6833447

GENERAL INPORMATION:
APPLICANT: Goldman, Barry S.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Wisgand, Roger C.
TITLE OF INVENTION: Myxococcue xanthus Genome Sequences and Uses Thereof
FILE REFERENCE: 38-10(15849)B
CURRENT APPLICATION UNMBER: US/09/902,540
CURRENT APPLICATION NUMBER: 60/217,883
PRIOR FILING DATE: 2000-07-10
PRIOR FILING DATE: 2000-07-10
NUMBER OF SEQ ID NOS: 16825
SEQ ID NO 1096
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1419 GTCCCCTGGCAGGAGGAACCGGGAGGATGGCTACCTCTCGGGGCTCAATAACCTCGTC 1478
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Matches:
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LOCATION: (1)..(14555)
OTHER INFORMATION: unsure at all
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US-09-902-540-1096/c
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	391 164 164 177 177 192 212 212 212 232	245 265 265 265 265 SULT 13 SULT 13 -09-016-434 -09-016-434 APPLICANT APPLIC
Qy 57 ValProAlaArg1leArgAspThr	RESULT 12 US-09-252-991A-12872/C US-09-252-991A-12872/C Squence 12872, Application US/09252991A Patent No. 6551795 GENERAL INFORMATION: TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS TITLE OF INVENTION: US AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS TITLE OF INVENTION: US 60/074, 788 FILE REFERENCE: 107196.136 CURRENT FILING DATE: 1998-02-18 PRIOR FILING DATE: 1998-02-18 PRIOR PELLING DATE: 1998-07-27 NUMBER OF SEQ ID NOS: 33142 SEQ ID NO 12872 LENGTH: 984 TYPE: DATA ORGANISM: Pseudomonas aeruginosa US-09-252-991A-12872	Alignment Scores: Pred. No.: 107.50 Matches: 91 Score: 107.50 Matches: 91 Secret: 107.50 Matches: 91 Secret: 107.50 Matches: 91 Secret: 107.50 Matches: 91 Secret: 107.50 Matches: 91 Mismatches: 117 Mismatches: 117 Mismatches: 118 Mismatches: 118 Mismatches: 119 Mismatches: 110 Mismatches: 117 Mismatches: 118 Mismatches: 118 Mismatches: 119 Mismatches: 119 Mismatches: 110 Mismatch

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|102 CGCCCAGGCCGCCCGGGCCGCAAGCCGGAACACATACGTGGCCCCCTTGTGCA 2643
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                                                                                                                                                                                                                                                                                                                                                                                                                 gValLeuArgArgTyrValSerSerValAlaAsp------GluGlyMetAspCy 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        240 -GlyvalThrvalLysLeuvalAspPheAlaHisValAlaGluGlyAspGlyValIleAs 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     pHisAsnPhereu-----GlyGlyLeuCysSerLeuIleLysPheValSe 274
                                                                                                                                                                                                                           186 sAlaieuAlaAlaAlaValTyrGlyGlyLysGlyGlyValieuSerGlnLeuArgGluLe
                                                                                                        1642 GÉCÉTGATGCCGTGTAGCGGTCCTCGGAGGCCGGGAACTCCAGGGTGGCCAGGGGCGTCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2369 CGGTCTCAGGCTGCAAGTTTGTGAT---GACCATCTCCTG------GGCATCGGCCA
                                                                                                                                                                                                                                                                                                             206 uLysAlaTrpPheGluGluGln---ThrLeuPheHisPheTyrSerAlaSerIleLeuLe
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APPLICANT: RODAN, GIDEON A.
APPLICANT: SCHMIDT, AZRIEL
APPLICANT: STUTLEDGE, SU JANE
TITLE OF INVENTION: CDNA ENCODING A NOVEL HUMAN PROTEIN
TITLE OF INVENTION: TYROSINE PHOSPHATASE
NUMBER OF SEQUENCES: 7
CORRESPONDENCES ADDRESS:
ADDRESSSE: J. MARK HAND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2261 GGACCTGGTAGCCGCGGATCTGGCCGTGCTGCCGGGCCGGG 2222
                                                                                                                                                                                                                                                                                                                                    2473 -CAGGGTTGGGCGGCCCAGCACTGCTCCCTTGGTCACAACCAC-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     274 rAspIleValProGluThrProHisThrGlnProLeuGly 287
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: PAPLICATION NUMBER: US/08/348,006B FILING DATE: CLASSIFICATION: 514 PRIOR APPLICATION DATA: PRIOR APPLICATION DATA: APPLICATION NUMBER: US 08/122,032 FILING DATE: 14-SEP-1993 ATTONNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         E: J. MARK HAND
126 E. LINCOLN AVE., P.O. BOX 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 6, Application US/08348006B Patent No. 5658756
                                                                  161 salaMetAspThrAlaGlyVal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: RAHWAY
STATE: NEW JERSEY
COUNTRY: USA
ZIP: 07065-0900
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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TELEPHONE: 908-594-3905
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CITY: RA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          96 yPheGlnAlaProCysValAlaAspIleLysIleGlyAlaIleThrTrpProProSerSe 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      116 rProGluProTyrIleAlaLysCysLeuAlaLysAspArgGlyThrThrSerValLeuLe 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   --------GlyProGluGlyAlaValTrpArgThrGluArgProGluValLy 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                55 ------AlaAlaValProAla-ArgIleArgAspThrPhePheProArgPheHi 70
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16 AlaSerAlaSerLysLeuGlyProLeu---IleAspGlySerGlyLeuPheTyrLysPro 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  35 LeuGlnAlaGlyAspArgGlyGluHisGluValAlaPheTyrGluAlaPheSerAlaHis
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
ODERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Mord Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/016,434
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Matches:
Conservative:
Mismatches:
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                                                                                                                                                                                                                     CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: 77,071
TELECOMONICATION INFORMATION:
TELEPHONE: (650) 845-4166
INFORMATION FOR SEQ ID NO: 1132:
SEQUENCE CHARACTERISTICS:
LENGTH: 4078 base pairs
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107.50
33.53$
24.25$
                                                                                                                       HEREWITH
                                                                                                                       FILING DATE: HEREWITH
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: nucleic acid
STRANDEDNESS: single
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IMMEDIATE SOURCE:
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CLONE: 91407624
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Best Local Similarity:
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DB:
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                          240 -GlyValThrValLysLeuValAspPheAlaHisValAlaGluGlyAsp---GlyValIl
                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 6, Application US/08800825A
Patent No. 5866397
GENERAL INFORMATION:
APPLICANT: SCHNIDT, AZRIEL
APPLICANT: RUTLEDGR, SU JANE
TITLE OF INVENTION: TYROSINE PHOSPHATASE
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: J. MARK HAND - MERCK & CO., INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3077 AGTICITGGGCGAGACITGGICCCGCAGGAACGICCGGIAGCGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-10-042-894A-8 (1-289) x US-08-800-825A-6 (1-6000)
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126 E. LINCOLN AVE., P.O. BOX 2000
                                                                                                                                                                                                                                                                                                                 2249 CGCGGATCTGGCCGTGCTGCCGGGCCGGG 2222
                                                                                                                                                                                                                                                           278 oGluThrProHisThrGlnProLeuGly 287
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APPLICATION DATA:
APPLICATION NUMBER: US/08/800,825A
FILING DATE: 14-FEB-1997
CLASSIPICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: HAND, J. MARK
REGISTRATION NUMBER: 36,545
REFERENCE/DOCKET NUMBER: 18992DA
TELECOMMUNICATION INFORMATION:
TELEPHONE: 73-2594-33955
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33.64%
24.24%
7.00%
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TELEFAX: 732-594-4720
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: nucleic acid
STRANDEDNESS: single
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ZIP: 07065-0900
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: 126 E
CITY: RAHWAY
STATE: NEW JEJ
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TGGGTTTGCTGCGAGCGCCATCGCCCTTCATGGTGTAGGCGGCTACCGTGATGGAGTACG 2370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -----GGCCCCGTTGCGCTCGGCGCACGGGTGGCAGCCAGCGGA 2802
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2762 GAATCTGCGGGTGGCCACGGGGCGTGTCCTCCGGGATGCTCAGGACCTCGGCTGCCTCCT 2703
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2702 cocccagoccocccosocricidesocosoaagocosaacacaracorosocicicerrerida 2643
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2582 AGTCCTCACGGCCAAACTGCAGGGGGTAGCCCAGCACCTGGTCCTCCGGGGTGCCAGCCG 2523
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           96 yPheGlnAlaProCysValAlaAspIleLysIleGlyAlaIleThrTrpProProSerSe 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             116 rProGluProTyrIleAlaLysCysLeuAlaLysAspArgGlyThrThrSerValLeuLe 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gyalLeuArgArgTyrValSerSerValAlaAsp------GluGlyMetAspCy 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              186 sAlaLeuAlaAlaAlaValTyrGlyGlyLysGlyGlyValLeuSerGlnLeuArgGluLe 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             206 uLysAlaTrpPheGluGluGlu---ThrLeuPheHisPheTyrSerAlaSerIleLeuLe 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -------GlyProGluGlyAlaValTrpArgThrGluArgProGluValLy 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         54
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16 AlaSerAlaSerLysLeuGlyProLeu---IleAspGlySerGlyLeuPheTyrLysPro 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            35 LeuGlnAlaGlyAspArgGlyGluHisGluValAlaPheTyrGluAlaPheSerAlaHis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -------GlyGluProHisProHisLeuValLeuAspAspLeuLeuAlaGl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  891 CAGGGCCCAGGGCACCGGCCTCCCGCACGGCCACCGTGTATTTGACGAT-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         136 uGlyPheArgValSerGlyValArgValVal------
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SEQUENCE CHARACTERISTICS:
LENGTH: 6000 base pairs
                                                                                                                                                                                                                                                              0.251
106.50
33.64%
24.24%
                       LENGTH: 6000 base pair:
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
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Aac49750 Arabidops
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Aad43520 Maize ino
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/product= "Maize IPPK protein #4"
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AAD43515
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ABL23306
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AAD53176
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AAD43514
        Command line parameters:
-MODEL=frame+ p2n.model-DEV=xlh
-Q=/Cqn2_1/USPTO_spool/US10042894/runat_15062005_111949_8281/app_query.fasta_1.455
-Q=/Cqn2_1/USPTO_spool/US10042894/runat_15062005_111949_8281/app_query.fasta_1.455
-Q=/Cqn2_1/USPTO_spool/US10042894/runat_15062005_111949_8281/app_query.fasta_1.455
-DB=N Geneseq_16Dec04 -QFMT=fastap -SUFFIX=p2n.rng -MINNATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 - MATRIX=blosum62 -TRANS=human40.cdi
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 - THR MAX=100 -THR MINSO -ALIGN=15
-MODE=LOCAL -OUTFMT=pto -NORM-ext -HEAPSIZE=500 -MINLENE-0 -MAXIEN=200000000
-USER=US10042894_@CGN 1 1_470 @runat_15062005_111949_8281 -NCPU=6 -ICPU=3
-NO MMAP -LARGEQUERY -NRG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
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Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                      - nucleic search, using frame plus p2n model
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Listing first 45 summaries
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The invention relates to novel inositol polyphosphate kinase (IPPK) polypeptides and polymucleotides. Sequences of the invention are useful in modulating the phytic acid biosynthesis by decreasing phytate and/ or increasing non-phytate phosphorous to improve the nutritional value of animal feed, or to reduce the environmental impact of animal waste. Polymucleotides of the invention are to produce transgenic plants with an altered phenotype. IPPK proteins are used to screen compounds that modulate their activity and raising anti-idiotypic antibodies. The present sequence is maize IPPK DNA
                                                                                                                                                ValThrValLysLeuValAspPheAlaHisValAlaGluGlyAspGlyValIleAspHis 260
GACGAGGGGATGGACTGTGCGCTCGCCGCGGTGTACGGAGGAAAAGGTGGAGTCTTG 651
                                           GTGACGGTGAAGCTGGTGGACTTTGCCCCATGTGGCCGAGGGTGATGGGGTGATTGACCAC
                             SerGlnLeuArgGluLeuLysAlaTrpPheGluGluGlnThrLeuPheHisPheTyrSer
                                                                                       AlaSerIleLeuLeuGlyTyrAspAlaAlaAlaValAlaAlaGlyGlyGlyGlyGlyGlyGly
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                                                                                      New inositol polyphosphate kinase polynucleotides and polypeptides, useful in modulating phytic acid biosynthesis by decreasing phytate increasing non-phytate phosphorous to improve the nutritional value animal feed.
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               Rafalski
                                                                                                                                                               Claim 1; Page 64-65; 86pp; English.
                                                                                                                                                                                                                                                                                                                    present sequence is maize IPPK DNA
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The invention relates to novel inositol polyphosphate kinase (IPPK) polypeptides and polynucleotides. Sequences of the invention are useful in modulating the phytic acid blosynthesis by decreasing phytate and/ or increasing non-phytate phosphorous to improve the nutritional value of animal feed, or to reduce the environmental impact of animal waste. Polymucleotides of the invention are to produce transgenic plants with an altered phenotype. IPPK proteins are used to screen compounds that modulate thair activity and raising anti-idiotypic antibodies. The present sequence is maize IPPK DNA
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nutritional value; animal feed; transgenic; gene; ds
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                      AAD43512 standard; DNA; 923
                                                                    (first entry)
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P-PSDB; AAE26194.
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Rafalski JA,
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                                                                                                                                                                                                                                                                                                                                                                                                                                   present sequence is maize IPPK DNA
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sAsnPheLeuGlyGlyLeuCysSerLeuIleLysPheValSerAspIleValProGluTh 280
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P-PSDB; AAE26201.
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ATGCCCGACCTCCACCCGCCGGAGCACCAAGTCGCCGGTCACCGCGCCTCCGCCAGCAAG 148
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New inositol polyphosphate kinase polynucleotides and polypeptides, useful in modulating phytic acid biosynthesis by decreasing phytate increasing non-phytate phosphorous to improve the nutritional value animal feed.
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Maize, enzyme, inositol polyphosphate kinase, IPPK; phytic acid;
nutritional value, animal feed; transgenic; ds.
                                                                                                                                                 Maize inositol polyphosphate kinase (IPPK)
                                                                                            BP.
                                                                                            AAD43519 standard; DNA; 643
                                                       rccrragacccac 886
                                      rProHisThrGln 284
                                                                                                                                (first entry)
                                                                                                                                14-NOV-2002
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MetSerAspLeuHisProProGluHisGlnValAlaGlyHisArgAlaSerAlaSerLys

Conservative: Mismatches: Indels:

Percent Similarity: Best Local Similarity: Query Match:

Gaps:

US-10-042-894A-8 (1-289) x AAD43518 (1-899)

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The invention relates to novel inositol polyphosphate kinase (IPPK) polypeptides and polynucleotides. Sequences of the invention are useful in modulating the phytic acid biosynthesis by decreasing phytate and/ or increasing non-phytate phosphorous to improve the nutritional value of animal feed, or to reduce the environmental impact of animal waste. Polynucleotides of the invention are to produce transgenic plants with an altered phenotype. IPPK proteins are used to screen compounds that modulate their activity and radising anti-idiotypic antibodies. The present sequence is P. argentatum IPPK DNA
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Enzyme, inositol polyphosphate kinase, IPPK, phytic acid, transgenic,
nutritional value, animal feed, gene, ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New inositol polyphosphate kinase polynucleotides and polypeptides, useful in modulating phytic acid biosynthesis by decreasing phytate increasing non-phytate phosphorous to improve the nutritional value animal feed.
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P-PSDB; AAE26199.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               present sequence is maize IPPK DNA
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                                                                                                                                       (PION-) PIONEER HI-BRED INT INC
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                                                                          64 ThrephephoproArgPheHisGlyThrArgLeuLeuProThrGluAlaGlnProGlyGlu 83
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                                                   144 GAAGTAGCTTTTATGAATCATTTTCTTCTAACAATAATATTCCAGAACACATACG---
                                                                                     AAATTCTTTCCTATATATATGGCACCAAAATCATG-----AAGGCATCCACTGGCTCT
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nutritional value; animal feed; gene; ds.
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                                        143 ValArgvalval --- GlyProGluGlyAlaValTrpArgThrGluArgProGluValLys 161
                                                                                                                                                182 GluGly-------MetAspCysAlaLeuAlaAlaAlaValTyrGlyGlyLysGly 197
                                                                                                                                                                                                                                                           237
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                                                                                                                                                              530 CTAAGGGTATATCAAAATAGCGAAGCTGGATTTTTGGCAACCTGAGAAGAAGGTTGTTAT
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ò	24 LeulleAsp	GlySerGlyLeuPhe	eAspGlySerGlyLeuPheTyrLysProLeuGlnAlaGlyAspArgGl	AlaGlyAspArgGlyGluHis	43
q	154 CTCGTAGA	 	:: CTCGTAGATGACCAAGGCCGGTTCTTCAAGCCACTTCAGGGAGATTCTCGTGGC	GGAGATTCTCGTGGCGAACAC	213
ò	44 GluvalAle	PheTyrGluAlaPhe	SerAlaHisAlaAla	GluValAlaPheTyrGluAlaPheSerAlaHisAlaAlaValProAlaArgIleArgAsp	63
д	214 GAGGCTAAC		: : : : : : : : : : : : : : : : : : :	 GAGGCTAAGTTCTATGAGTCTTTCACATCGAACATGAAGGTTCCAGATCACCAT	270
ò	64 ThrPhePhe	ProArgPheHisGly	ThrArgleuleuPro	ThrPhePheProArgPheHisGlyThrArgLeuLeuProThrGluAlaGlnProGlyGlu	83
q	271 AGATACTT	::: AGATACTTCCCGGTGTATCACGGCACTCAGCTAGTT-	-	GAAGCATCTGATGGATCT	324
λō	84 ProHis	-ProHisLeuValLeu	1AspAspLeuLeuAla	-ProHisLeuValLeuAspAspLeuLeuAlaGlyPheGlnAlaProCysVal	102
q	325 GGCAAGCT	rcrcarcrrgrrcrr		GGCAAGCTICCTCATCTIGITCTIGATGATGATGTTTCAGGGTACGCAAACCCGTCGGTA	384
ò	103 AlaAspile	PLYBILEGLYALAILE	ThrTrpProProSer	AlaAspIleLysIleGlyAlaIleThrTrpProProSerSerProGluProTyrIleAla	122
qa	385 ATGGATGT	TAAGATTGGATCTAGG		ATGGATGTTAAGATTGGATCTAGGACATGGTACCGGGATGTATCAGAAGAATACTTCAAG	444
ò	123 LysCysLer	AlaLysAspArgGly	ThrThrSerValLeu	SLeuAlaLysAspArgGlyThrThrSerValLeuLeuGlyPheArgValSerGly	142
qq	445 AAATGTAT	FAAGAAAGATAGACAG	ACCACCACGGTTTCG		504
ò	143 ValArgVa	ValGlyProGlu	GlyAlaValTrpArg	ValargValValGlyProGluGlyAlaValTrpArgThrGluArgProGluValLy8	161
ପ୍ପ	SOS TTTAAGAT	: FTTTGATCACCAAGAA	.:: ATCAAGTTTTTGGAGA	TTAAGATTTTTGATCACCAAGATCAGTTTTTTGGAGAGCTGAGAAGAAGCTTGTTCTT	564
'n	162 AlaMetAsp	ThrAlaglyValArg	rg.	TyrvalserServal	179
දු	565 GGGTATAA	: rgcagargfrgctaga	ATTGGCTCTGAGGAAG	GGGTATAATGCAGATGGTCTAGATTGGCTCTGAGGAAGTTTGTGTCATCGAACTCTCCCC	624
ò	180 AlaAspGluGlyMet		-AspCysAlaLeuAlaAlaAlaAlaValTyrGlyGl	AlaValTyrGlyGlyLysGly	197
qa	625 GCTGACTC	TAACTTGACACCAAAC	CTGTGCTTTTGCATCA	CTGACTCTAACTTGACACCCAAACTGTGCTTTTGCATCAGAGGTTTATGGGGGTTGTAAC	684
ò	198 GlyValLer	JSerGlnLeuArgGlu	1LeuLysAlaTrpPhe	GlyValLeuSerGlnLeuArgGluLeuLysAlaTrpPheGluGluGluGlnThrLeuPheHis	217
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0y 2,	4 LeulleAsp	GlySerGlyLeuP	neTyrLysProLeuGln	LeulleAspGlySerGlyteuPheTyrLysProLeuGlnAlaGlyAspArgGlyGluHis	43
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32;	S GGCAAGCTT	CTCATCTTGTTCT	TGATGTTGTTTCA	::: GGTACGCAAACCCGTCGGTA	384
10		Lygileglyalai]	eThrTrpProProSer	AlaAspileLysileGlyAlaileThrTrpProProSerSerProGluProTyrileAla	∾ .
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DP 20		TTTGATCACCAAG	ATCAAGTTTTGGAGAC	SCTGAGAAGAAGCTTGTTCTT	Ġ.
Qy 163	2 AlaMetABD	ThralaglyValA	cgArgValLeuArgArgC	AlaMetAspThrAlaGlyValArgArgValLeuArgArgTyrValAlSerSerVal	179
e e		9CAGA1 9G19C1A	anticocici caccana	וופופורשורפשערופורר	
Oy 18(0 AlaAspGlu 5 GCTGACTCT	GlyMetA& ::: AACTTGACACCAA	ppCysAlaLeuAlaAla/ :: \crGrGcTTTTGCATCA(AlaAspGluGlyMetAspCysAlaLeuAlaAlaAlaValTyrGlyGlyLysGly GCTGACTCTAACTTGACACCCAACTGTGCTTTTGCATCAGAGGTTTATGGCGGTTGTAAC	197
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The invention relates to novel inositol polyphosphate kinase (IPPK) polypeptides and polymucleotides. Sequences of the invention are useful in modulating the phytic acid biosynthesis by decreasing phytate and/ or increasing non-phytate phosphorous to improve the nutritional value of animal feed, or to reduce the environmental impact of animal waste. Polynucleotides of the invention are to produce transgenic plants with an altered phenotype. IPPK proteins are used to screen compounds that modulate their activity and raising anti-idiotypic antibodies. The
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                                                                                                                                                                          Soybean; enzyme; inositol polyphosphate kinase; IPPK; phytic acid; nutritional value; animal feed; transgenic; gene; ds.
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DNA; 1105
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103 AlaAspIleLysileGlyAlaIleThrTrpProProSerSerProGluProTyrIleAla 122
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||||CTCARGE-----GACTCTATCTCCTGGGAACCTACCAGGAAATCTCTCCCAGTGT 485
                                                                                                                                                                                  163 MetAspThrAlaGlyValArgArgValLeuArgArgTyrValSerSer----- 178
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                                                                                                                                                                                                                         ---CCCCACCCTCACCTGGTCCTGGAGCACCTCTGCGGGCTACTCCAAACCCTCCGTC 314
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
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AUTHORS
TITLE
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-Q=/cgn2_1/USPTO_spool/US10042894/runat_15062005_111950_B208-1-LoOPCL=0_-LOOPEXT=0_-LONITS=bits_0-START=1_-END=-1_-MATRIX=blosum62_-TRANS=human40_cdi_-LIST=45_-LOOFALIGN=200_-TRR_SCORE_BEDCT_-TRR_MAX=100_-TRR_MIN=0_-ALIGN=15_-MODE=LOCAL_-COUTEWT=pto_-NORM==&t_-HEAPSIZE=50_-WINTEN=0_-MAXLEN=200000000_-USER=US10042894_@CGN_1_1_3731_@runat_15062005_111950_8289_-NCPU=6_-ICPU=3_-NORM=-LARGEQUERS_-NGS_SCORES=0_-WAIT--DSPELOCK=100_-LONGLOG_-TCPU=3_-LOEV_TRREOUT=120_-WARN_TIMEOUT=130_-TRREOUT=120_-WARN_TIMEOUT=120_-WARN_TIMEOUT=120_-TRREOUT=120_-TRREOUT=120_-TRREOUT=120_-TRREOUT=120_-TRREOUT=120_-TRREOUT=1_-TRREOUT=120_-TRREOUT=120_-TRREOUT=120_-TRREOUT=120_-TRREOUT=120_-TRREOUT=120_-TRREOUT=120_-TRREOUT=120_-TRREOUT=120_-TRREOUT=10_-TRREOUT=120_-TRREOUT=120_-TRREOUT=120_-TRREOUT=120_-TRREOUT=10_-TRREOUT=120_-TRREOUT=120_-TRREOUT=120_-TRREOUT=120_-TRREOUT=10_-TRREOUT=120_-TRREOUT=120_-TRREOUT=120_-TRREOUT=120_-TRREOUT=10_-TRREOUT=120_-TRREOUT=120_-TRREOUT=120_-TRREOUT=120_-TRREOUT=10_-TRREOUT=120_-TRREOUT=120_-TRREOUT=120_-TRREOUT=120_-TRREOUT=10_-TRREOUT=120_-TRREOUT=120_-TRREOUT=120_-TRREOUT=120_-TRREOUT=10_-TRREOUT=120_-TRREOUT=120_-TRREOUT=120_-TRREOUT=120_-TRREOUT=10_-TRREOUT=120_-TRREOUT=120_-TRREOUT=120_-TRREOUT=120_-TRREOUT=10_-TRREOUT=120_-TRREOUT=120_-TRREOUT=120_-TRREOUT=120_-TRREOUT=10_-TRREOUT=120_-TRREOUT=120_-TRREOUT=120_-TRREOUT=120_-TRREOUT=10_-TRREOUT=120_-TRREOUT=120_-TRREOUT=120_-TRREOUT=120_-TRREOUT=10_-TRREOUT=120_-TRREOUT=120_-TRREOUT=120_-TRREOUT=120_-TRREOUT=10_-TRREOUT=120_-TRREOUT=120_-TRREOUT=120_-TRREOUT=120_-TRREOUT=10_-TRREOUT=10_-TRREOUT=10_-TRREOUT=10_-TRREOUT=10_-TRREOUT=10_-TRREOUT=10_-TRREOUT=10_-TRREOUT=10_-TRREOUT=10_-TRREOUT=10_-TRREOUT=10_-TRREOUT=10_-TRREOUT=10_-TRREOUT=10_-TRREOUT=10_-TRREOUT=10_-TRREOUT=10_-TRREOUT=10_-TRREOUT=10_-TRREOUT=10_-TRREOUT=10_-TR
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AX513564 Sequence
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                              GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                         nucleic search, using frame_plus_p2n model
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AX513578 Sequence AP006772 Oryza sat AK072296 Oryza sat AX513580 Sequence AX513576 Sequence AX513576 Sequence AX513576 Sequence AX513574 Sequence AX513573 Arabidops AY072621 Arabidops AY072621 Arabidops AY085862 Arabidops AY136378 Arabidops AY135378 Arabidops AX135378 Arabidops AX13592 Sequence AX513592 Sequence AX513593 Drosophil AC008002 Drosophil AC008002 Drosophil AX116726 Ciona Int BC001124 Xenopus 1 CQ771531 Sequence

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KAMDTAGVRRVLRRYVSSVADBGMDCALAAAVYGGKGGVLSQLRELKAMFEEGTLFHP
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YSASTILGYDAAAVAAGGGGGGGVTVKLVDFAHVAEGDGVIDHNFLGGLCSLIKFVSDI
VPETPQTQPLGPS"
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Spermatophyta, Magnoliophyta, Liliopaida, Poales, Poaceae, PACCAD
clade, Panicoideae, Andropogoneae, Zea.
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Sequence 5 from Patent W002059324.
AX513568.1 GI:23559668
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        ProGlyGluProHisProHisLeuValLeuAspAspLeuLeuAlaGlyPheGlnAlaPro

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Sequence 1 from Patent W002059324.
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Shi,J., Beach,L.R., Wang,H., Rafalski,J.A. and Cahoon,R.E.
Novel inositol polyphosphate kinase genes and uses thereof
Patent: WO 02059124-A 20 01-AUG-2002;
PIONEER HI-BRED INTERNATIONAL, INC. (US)
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Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACCAD
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Spermatophyta, Magnoliophyta, Liliopaida, Poales, Poaceae, PACCAD
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   CTGGGCCCACTCATCGACGACTCTGGCCTCTTCTACAAGCCGCTCCAGGCCGGCGACCGT
                                                                                                                                                             Shi,J., Beach,L.R., Wang,H., Rafalski,J.A. and Cahoon,R.E. Novel inositol polyphosphate kinase genes and uses thereof Patent: WO 02059324-A 15 01-AUG-2002; PIONEER HI-BRED INTERNATIONAL, INC. (US) Location/Qualifiers
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/product="putative ubiquinol-cytochrome c reductase
iron-sulfur subunit, mitochondrial precursor"
/potealnid="BAD26134.1"
/db_xref="c1:4388912"
/translation="MLRVAGRRLTTALAWRPAAAAGARGPLAGGSLPGDDEFSREPQR
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TTYTVKRRGKPVFIRRRIFEDINLANSVDIGSLRDPQDABENKNDEWLVIGCTHL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /trānslation="menatvtaadlapwsQQCRPvGEEEEGGVaaaaKKEEGRQIQKE
EKGGRRRGSGGIRKTM"
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complement (join(18932. .19648,19740. .19836,20081. .20194,
2020. .2044,20690. .20827,20923. .20999,21093. .21207,
21277. .21382,21703. .21764,21859. .21993,22149. .22331,
228890. .22936,23369. .23417,23504. .23652,24724. .24771,
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probably inactive due to including stop codon(s) in CDS"
join(15870. 16043,16479. 16484)
/gene="OSJNBa0047A17.5"
join(15870. 16043,16479. 16484)
/organism="Oryza sativa (japonica cultivar-group)"
mol type="ganomic DNA"
cultivar="Nipponbare"
db_xref="taxon:39947"
                                                                                                                                                                                                                                                                                                                                                                                                                                  complement (join(5864. .6755,8843. .9107))
/gene="OSJNBa0047A17.2"
/note="usported by full-length cDNA(s): AK102815"
/complement (join(6112. .6755,8843. .9017))
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complement(11599. .12180)
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/gene="OSJNBa0047A17.6"
/note="gupported by full-length cDNA(8): AK120851"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="Rieske iron-sulfur protein
contains EST(s): AU165272(C63256),AU068962(C51210)
contains full-length cDNA(s): AK102815"
                                                                                                                                                                                                                                                                                                                        predicted by GENSCAN
this category is not included in IRGSP standard"
complement(5864..9107)
/gene="OSJNBa0047A17.2"
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gone="GSDNBa0047A17.3"

join(<9904. .10067,10732. .>10750)

/gene="GSJNBa0047A17.3"
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/db_xref="G1:4938913"
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/gene="OSJNBa0047A17.1"
join(2637. .2780,3298. .3360)
/gene="OSJNBa0047A17.1"
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complement(<11599. .>12180)
/gene="OSJNBa0047A17.4"
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Direct Submission

Direct Submission

Submitted (18-SEP-2002) Takuji Sasaki, National Institute of Agrobiological Sciences, Rice Genome Research Program; Kannondai 21-12. Tsukubba, Idearki 305-8602, Japan In Carl 201-201.

Tel.801-208-38-7441, Fax:81-208-38-74468)

On Jun 28, 2004 this sequence version replaced gi:34740257.

Genes were predicted from the integrated results of the following: GENSCAN (http://ccm.oll.mit.edu/GENSCAN.html), FGENESH (http://ccm.oll.ology.gatech.old/Senskark), Glimmerh (http://cpm.olology.gatech.old/Senskark), Glimmerh (http://cpm.olology.gatech.old/Senskark), Glimmerh (http://cpm.olology.gatech.old/Senskark), SplicePredictor (http://www.tigr.org/db/glimmerm/glmr.form.html), RiceHWM (http://ycpm.olology.gatech.old/Senskark), SplicePredictor (http://ycpm.olology.gatech.old/Senskark), SplicePredictor (http://ycpm.olology.gatech.old/Senskark), SplicePredictor (http://ycpm.olology.gatech.old/Senskark), SplicePredictor (http://ycpm.olology.gatech.ology.plm.fcm.html), gap2 (http://www.tigr.org/software/glimmerm/) BanSYN and Electrican flow ology (http://www.tigr.org/software/glimmerm/) BanSYN and the coloning captoner was searched against NCBI NonRedundant Protein database with BanSYP. ESTS represent the identified cDNA sequences using BanSYN with the corresponding DBJ accession no. and RGP clone ID. Phil-length CDNAs represent the identified cDNA sequences using BanSYN with the corresponding DBJ accession no.

A gene with BanSYP ESTS represent the identified cDNA sequences using BanSYN with the corresponding DBJ accession no.

A gene with Admity or significant homology to a protein is classified based on the protein but with full-length of garrial such as same name, 'purcein and 'like protein', A gene predicted by capy protein but with full-length of any protein but with full-length of any protein but with full-length of any protein according to IRGSP standard. A gene predicted by a single gene prediction program is also classified as an 'hypochetical' protein accessio
                                                                                                                                                                                                                                                                                                                                       Oryza sativa (japonica cultivar-group) genomic DNA, chromosome 2, bac clone:OSJNBa0047Al7.
                                                            260 sAsnPheLeuGlyGlyLeuCysSerLeuIleLysPheValSerAspIleValProGluTh 280
                                                                                                 Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota, Viridiplantes, Streptophyta, Embryophyta, Tracheophyta;
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae,
         754 GGTAACAGTGAAGCTGGTGGACCTTGCCCATGTGGCCGAGGGTGATGGGGTGATTGACCA 813
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sasaki,T., Matsumoto,T. and Katayose,Y.
Oryza sativa nipponbare(GA3) genomic DNA, chromosome 2, BAC
clone:OSJNBa0047A17
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Direct Submission
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                                                                                SerAspLeuHisProProGluHisGlnValAlaGlyHisArgAlaSerAlaSerLysLeu
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218
21
39
5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length:
Matches:
Conservative:
Mismatches:
Indels:
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1148.50
84.45%
77.03%
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Pred. No.:
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                CDS
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Oryza sativa (japonica cultívar-group)

AP004772.3 GI:49388255

Percent Similarity: Best Local Similarity:

Query Match:

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10460. .10554,1077. .10826,10921. .11073,11145. .12275,
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TFPTLLPCYNBROWSILEDLEDLONGSTLASRALKFIOSMSLRDPLQPVGIIOECLSKCI
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COMDJement (16514., 23105)
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20914. 21120,21227. 21445,21564. 21638,21998. 22150))
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AU055859(S20105),AU085756(C52347),C27605(C52347),AU078722
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contains full-length cDNA(s): AK121782"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                contains full-length cDNA(s): AK065061, AK063159"
                                                                                                 note="start and end point are not identified"
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gene="P0415812.2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /codon_start=1
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              mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Agrobiological Sciences, Rice Genome Research Program; Kannondai 2-1-2 Tsukuba, Ibaraki 305-8602, Japan (E-mail:temasakianiae affer.go.jp, URL:http://rgp.dna.affer.go.jp/, GeneMark.html (http://www.softberry.com/), GeneMark.html), RiceHMM (http://rgp.dna.affer.go.jp/RiceHMM/), SplicePredictor (http://rgp.dna.affer.go.jp/RiceHMM/), SplicePredictor (http://www.tigr.org/software/glimmerm/), BLASTN and BLASTX. The genomic sequence was searched against NCBI NonRedundant Protein database at RGP or DDBJ. Protein homologies of the coding regions were searched against NCBI NonRedundant Protein database with BLASTR. Estr represent the identified cDNA sequences using BLASTN with the corresponding DDBJ accession no. and RGP clone ID. Full:hength cDNAs represent the identified cDNA sequences using BLASTN with the corresponding DDBJ accession no. and RGP clone ID. Full:hength cDNAs represent the identified cDNA sequences using BLASTN with the corresponding DDBJ accession no. and RGP clone ID. Full:hength cDNAs represent the identified cDNA sequences using BLASTN with the corresponding DDBJ accession no. and RGP clone ID. Full:hength cDNAs represent the identified cDNA sequences using BLASTN with the corresponding DDBJ accession no. and RGP clone ID. Full:hength cDNAs represent the identified cDNA sequences using Sunstfied based on the protesin name to indicate the homology to approach significant homology to any protein but with full-length cDNAs represent the entire EST homology (covering almost the entire length of partial sequence) is classified as an 'unknown' protein. A gene predicted by a single gene prediction program is also classified as a miscellaneous feature of the sequence is from the protein and is included by a single 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The orientation of the sequence is from SP6 to T7 of the PAC clone. This sequence of P0415B12 clone has an overlap with OSJNBa0047A17 clone (DDBJ: AP005749) at 5' end and an overlap with P045BB05 (DDBJ: AP004777) at 3' end. Detailed information on overlap and assembly quality together with annotation of this entry is available at http://rgp.dna.affrc.go.jp/GenomeSeq.html.
    Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    probably inactive due to including stop codon(s) in CDS probably inactive due to too long 3'UTR in CDS"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sasali,T., Matsumoto,T. and Yamamoto,K.
Direct Submission
Submitted (20-FEB-2002) Takuji Sasaki, National Institute of

    157419
    /organism="Oryza sativa (japonica cultivar-group)" /mol_type="genomic DNA" /cultivar="Nipponbare" /db xref="taxon:39947"
    /chromosome="2"

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                                                                                                                                                                                                                                         Sasaki,T., Matsumoto,T. and Yamamoto,K.
Oryza sativa nipponbare(GA3) genomic DNA,
                                                                                                                                                                                                                                                                                                                                                                            Published Only in Database (2002)
2 (bases 1 to 157419)
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                                                                                                                                                 Ehrhartoideae; Oryzeae; Oryza.
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                                                                                                                                                                                                                                                                                                                                     clone: P0415B12
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The Rice Full-Length CDNA Consortium, National Institute of
The Rice Full-Length CDNA Consortium, National Institute of
Agrobiological Science Rice Full-Length CDNA Project Team:,
Kikuchi,S., Satch,K., Nagata,T., Kawadashira,N., Doi,K.,
Kishimoto,N., Yazaki,J., Ishikawa,M., Yamada,H., Ooka,H., Hotta,I.,
Kojima,K., Namiki,T., Ohneda,E., Yahagi,W., Suzuki,K., Li,C.,
Ohtsuki,K., Shishiki,T., Foundation of Advancement of International
Science Genome Sequencing & Analysis Group:, Otomo,Y., Murakami,K.,
Ida,Y., Sugano,S., Fuljmura,T., Suzuki,Y., Taunoda,Y.,
Kurosaki,T., Kodama,T., Marudo,H., Kobayashi,M., Xie,Q.,
Narikawa,R., Sugiyama,A., Mizuno,K., Yokomizo,S., Niikura,J.,
Kusumegi,T., Oka,M., Ryu,R., Ueda,M., Matsubara,K., RIKEN:,
Kawai,J., Carninci,P., Adachi,J., Alzawa,K., RIKEN:,
Kawai,J., Carninci,P., Adachi,J., Alzawa,K., RIKEN:,
Hara,A., Hashidume,W., Hayatsu,N., Imotani,K., Ishii,Y., Itoh,M.,
                                                                                                                                                                                                                                                                                                                                                                                                                            10648 GGAAGCGGCGTGTAAGGGTGAAGCTGGTGGACTTCGCGCATGTCGACGATGGGGACGGG 40707
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PLI CDNA, CAP trapper.
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Bhrhartoideae; Oryzeae; Oryza.
---GlyGluProHisProHisLeuValLeuAspAspLeuLeuAlaGlyPheGlnAlaPro 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          220 SerAlaSerIleLeuLeuGlyTyrAsp-----AlaAlaAlaValAlaAlaGlyGly
                                                                                                                                                                SerGlyValArgValValGlyProGlu---GlyAlaValTrpArgThrGluArgProGlu
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                                                                                                                              CysvalalaaspileLysileGlyalaileThrTrpProProSerSerProGluProTyr
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                       / translation: "MASSTGAGGUERCKYKGYTSGDCLLINGSTKADVPPPEKSITLS
/ translation: "MASSTGAGGUERCKYKGYTSGDCLLINGSTKADVPPPEKSITLS
YLMAPRLARRGGUDEPAMESKEFLKKLCIGKEVTRYDYTAPNVGREFGTYLLGKN
VAYSIIAAGWARKKGGPFGEPSPYLTELLELEEVAKOGGLGRWSKEPGAAEESIRD
LPPSAIGEAGGFDAKGPAWAKGKSLEAIVEGYRDGSTYRYLLLESFOPTYTLGKU
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ETSINAHMERDFGHEAAVYLMDGLENSKRMDTRERKAALQNLEGFGKKKGRTQINQYGDVESDE
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|GCCCCGCTCGTCGACGCGAGGGCTCTTCTACAAGCCCCTCCAGGCCGGGAGCGCGGGG 40047
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complement(11727. .32496)
dene="P0415B12.7"
//pene="P0415B12.7"
//pene="P0415B12.7"
//pote="start and end point are not identified"
//pene="P0415B12.7"
//pene="P0415B12.7"
//pene="P0415B12.7"
//pote="elmilar to Oryza sativa chromosome7, P0404G11.101"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               62 ArgAspThrPhePheProArgPheHisGlyThrArgLeuLeuProThrGluAlaGlnPro 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'note="probably inactive due to including frameshift(s)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               probably inactive due to including stop codon(s) in CDS pseudogene, TNP2"
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/gene="P0415B12.5"
join(25322. .25357,28498. .28641)
/gene="P0415B12.5"
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/product="hypothetical protein"
/protein_id="BAD25377.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      | SerGlyvalArgValValGlyProGlu---GlyAlaValTrpArgThrGluArgProGlu 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ValLysAlaMetAspThrAlaGlyValArgValLeuArgArgTyrValSerSerVal 179
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NIAS Rice Full-Length cDNA Project Team: Kikuchi,S., Satoh,K.,
Nagata,T., Kawagashira,N., Doi,K., Kishimoto,N., Yazaki,J.,
Ishikawa,M., Yamada,H., Ooka,H., Hotta,I., Kojima,K., Namiki,T.,
Ohneda,E., Yahagi,W., Suzuki,K., Li,C., Ohtsuki,K., Shishiki,T. and Yamamoto,M.
Kagawa,I., Kondo,S., Konno,H., Miyazaki,A., Osato,N., Ota,Y.,
Saito,R., Sasaki,D., Sato,K., Shibata,K., Shinagawa,A., Shiraki,T.,
Yoshino,M. and Hayashizaki,Y.
                                                                                                                Collection, mapping, and annotation of over 28,000 cDNA clones from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (165-DEC-2001) Shoshi Kikuchi, National Institute of Agrobiological Sciences, Department of Molecular Genetics, Head of Laboratory of Gene Expression, 2-1-2 Kannondai, Tsukuba, Ibaraki 305-8602, Japan (E-mail:skikuchi@mas.affrc.go.jp, Tel:81-29-838-7007, Fas:81-29-838-7007)
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                                                                                                                                              japonica rice
Science 301 (5631), 376-379 (2003)
22752273
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ACCESSION VERSION KEYWORDS SOURCE ORGANISM

DEFINITION

source

PEATURES

REFERENCE AUTHORS TITLE JOURNAL

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     Parthenium argentatum
Parthenium argentatum
Parthenium argentatum
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheo;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots;
asterids; campanulids; Asterales; Asteraceae; Asteroideae;
Hellantheae; Parthenium.
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                                                        LeulleAspGlySerGlyLeuPheTyrLysProLeuGlnAlaGlyAspArgGlyGluHis
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rosids; Myrtales; Myrtaceae; Eucalyptus.
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GACATACTTTCGGAGACA 869
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                                                                                                                                                                                                                                                                                                                                                                                                                                         AX513574.1 GI:23559674
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722.50
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52.84
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ACCESSION
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SOURCE
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AX513574
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DNA linear PLN 24-JAN-2002 Ngc-D, Ngc-A and Ngc-B genes.

Score:

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/ LEANT LONG POWER TO THE CONTRIBUTION OF THE 
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/gene="Ngc-B"
join(20265. .20815,21104. .22202,22415. .22690,22818. .24218)
/gene="Ngc-B"
                                                                                                                                                                                                                                                                                                                                                                                                                                              .14542,14757. .15032,15186. .16493)
/product="hypothetical protein"
/protein id="CAC35324.1"
/db_xref="GA[31.13509210"
/db_xref="GA].09ARC1"
/db_xref="CAC354RC1"
/db_xref="CAC354C1"

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/product="Ngc-B protein"
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/protein_id="CAC35325.1"
/db_xref="G1:13509211"
/db_xref="G1:13509211"
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/db_xref="UniProt/TrEMBL:09AR40"
/tb_xref="UniProt"
/tb_xref="UniProtPropEGIGNGETIGSSUDPTLPLLPSGEYEVFLSFRGPDVRO
Tranblation="WMRSDTDSSIGSFLSRSSVDPTLPLLPSGEYEVFLSFRGPDVRO
TranblatyAMLYARKIFFRDEEGIGNGETIGSSLIQATTESKIYIPILTQNYASSKWC
LQELAKMYDCWKNGGGGGKGQHIILPVFYFMDPRDVRHPDSGPYKEAFEQHNLKHDPET
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/gene="NgC-A"
join(12668. .13218,13450. .14542,14757. .15032,1518
/gene="NgC-A"
/note="N rust resistance gene homolog: TIR-NBS-LRR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /codon_start=1
/product="Ngc-A protein"
/protein id="CAC35323.1"
/db_xref="GI:1359299"
/db_xref="GGA:Q9ARC2"
/db_xref="GDA:Q9ARC2"
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TRADHLYTSLVRSKERTFRDBEELBKGGTIGPSLIRALTESKY IN INTERPRESESSWC
LQBELAKWGCWKSGCAKGQHILLIPVPLFVDRDWRHTESGSYKEAFEBHSQKHDPET
ULBWKEALQBYGBKKGYHYTESDGHGSIIDKILTEVELHIGANYALVTDBLVGTDSRV
DEVVGLINDSSTSEKIIGIHGWGGLGKTTLAKAVYDKVSTKFERCYFLENIRDTLSE
KNOYSILQNKIISGILIKRDPREAKNANDGIRIIRDRYKSTKFERCYFLENIRDTLSE
KNOYSILQNKIISGILIKRDPREAKNANDGIRIIRDRYBDSLYLTLFNKHAFDVDCPPK
DYALLSKEFVQAAAGLPLYIKVIGSLLERMOKIFWEEKLEFKKISPTKVQERLKISY
NELTHNEKQIFLDTACYFIGSQKIYPIFFWERKLEFKKISPTKVQERLKISY
ONGGEDLILTNKEFWELTHRRYLYKSKRRIIRSNGAVPKRARIIKKKYQFUCVEVLT
VDNGGEDLILTNKEFEKTHRRYLYKSNARLAGDFKDVLPWLLLESCDSVESGLY
LKKLVRLDLHDCSVGDSWKGWNELKVARKLAGDFKDVLPWLESCDSVESGLY
LKKLVRLDLHDCSVGDSWKGWNELKVARKLAGVSKKCPPIKKVVPDFSDCGDLEFLNF
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SKLSSLEFLALALTDSYKSDFTEMLPTSLTLLYISNDTQKFCPDTSSENLQRLPNLSN
LINLSVLYLIDVGIGEILGLGELKMLEYLSIGRASRIVHLDGLENLVLLQHLRVEGCR
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ELI EVPGLDALESLKWLSMEGCRSTRKVPDLSGLKKLKTLDVESCIQLKEVRGLERLE
SLEELKMSGCESI EELPNLSGLKNLRELLLKGCIQLKEVNGLEGLELTVFEARKRIKA
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                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (22-MAR-2001) Dodds P.N., Plant Industry, CSIRO, GPO Box 1600, Canberra, ACT 2601, Australia Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /gene="Ngc-D"
/standard_name="n-X50"
/note="Site_of 11 bp insertion in n-X50 rust susceptible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /grandard_name="n-X128A"
/note="SiTe of LUTE transposon insertion in n-X128A rust
susceptible mutant allele"
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/note="233 bp deletion in n-X139 rust susceptible mutant
Dodde, P.N., Lawrence, G.J. and Ellis, J.G.
Contrasting modes of evolution acting on the complex N locus for
rust resistance in Flax
Plant J. 27 (5), 439-453 (2001)
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/gene="Ngc-D"
join(2881. .3431,3533. .4652,4770. .5045,5140. .6519)
/gene="Ngc-D"
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/protein id="CAC35321.1"
/db_xref="G1:1359920"
/db_xref="G0.29ARC4"
/db_xref="UniProt/TrEMBL:Q9ARC4"
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/product="hypothetical protein"
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/mol type="genomic DNA"
/varlety="Bombay"
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/haplotype="N"
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/function="unknown"
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115/6428
2 (bases 1 to 25054)
Dodds, P.N.
Direct Submission
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US-10-042-894A-8 (1-289) x ATH243592 (1-903)
221 AlaSerIleLeuLeuGlyTyr-
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Pred. No.:
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DEFINITION
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                              NDGWYALQWKYI SDILKAGONGARAASDGWA I TRERVARHKI FWYLDDI DESFRIPDE I FGKLGDESFRENCE LEGET I TYRDARTIELIANGKWFRIKT FWYLDDI DESFRIPDE I FGKLGDESFORSET I TYRDARTIELIANGKWFRENKI FWYLDDI DESFRIPDE I FGKLGDESFORSET I TYRDARTIELIANGKWFRENKE FWENKHENGY FRANCHENGY PREDVAL I ELKA I PSAKVQERLKWSY NELTHINEKO I FLDI ACLFVOARKEVPRWWSDCOLYPASTLETLYORGSTURMODNKKF WHEDHI RDIGRTI VREENSQNPYKR SRI WSNNDA I DI LKNREGNDCVBALRYDWKGEG YALTWEFKQFSKR RE-EULMGAGLSGNFKNII LDANGKATVAYRORGSPS PSGLILNKAVI LELGCYVTHSWKGMEI LAAGKLKWVNITSGG I LEKYPDLSTCRGLELLCFHKCQWWR GELDIGTFKDLKVLDINQTEI TTLKGEVESLQNLQQLDWGRSGLI EVPAGI SKLSSLE FLDLIKWYGNED HAAGKLKWVNITSGG I LEKYPDLSTCRGLELLCFHKCQWWR GELDIGTFKDLKVLINGKLENDINGKLENLGFHKCQWWR GELDIGTFKDLKVINGKLENLGHLENCOWNG LTRLLKEVGI HEI PGLGKLKLLESLSI CTAPALDISDLGENLVLLKELAERDE PRILASLE GTLUSSSLEKLENLESLENCONLGSI SCHADLINGKNELLENG GTLVSSGFELTWILDLSLESLSI GORDNLOGDSLSHLDI SWCPRLTVNDLLHGLLKLGGTLSLESLESLGSTONLGOSLSHLDI SWCPRLTVNDLLHGLLKLGGTLSLSLESLESLGSTONLGNSLSHLDI SWCPRLTVNDLLHGLLKLGGTLSLGGTLSLGGTLSLGGTLSLGGTSLGLGGTLSLGGTLSLGGTLSLGGTLSLGGTSLGGTLSLGGTSLGGTLSLGGTSLGGTSLGGTSLGGTSLGGTSLKLLKKTNTN SGCCSI KELPNLGSLKNUGLEELEWLDFNTDRRLKLKYLLKLV SRKGKQLVTGSARRALFINN"
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0156 TCGGACCAACCGGATTGTTCGTTTGCAGCGGTCGTTTACGGTGGTTCGAATGGGATCTTG 10215
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                162 AlaMetAspThrAlaGlyValArgArgValLeuArgArgTyrValSerSer---ValAla 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          146 ValGlyProGlu------GlyAlaValTrpArgThrGluArgProGluValLy8 161
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10276 TGTTCTGTTCTTATGCTGTATGAGAAGAAGAAGACGAAGATGGTGAATGGAGAGAAGAGA 10335
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Arabidopsis thaliana gene for inositol-(1,4,5) trisphosphate
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----AspAlaAlaAlaValAlaAlaGlyGlyAspGly 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Xia,H.J., Brearley,C. and Mueller-Roeber,B.
Identification of inositol-(1,4,5) trisphosphate 3-kinase from
Arabidopsis thaliana
Unpublished
                                                                                                                                              -----GlyGlyValThrValLySLeuValAspPheAlaHisValAlaGluGlyAspGly
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Direct Submission
Submitted (09-JUL-1999) Xia H.J., AG Mueller-Roeber,
Max-Planck-Institute of Molecular Plant Physiology,
Karl-Liebknecht-Straese 25, Haus 20, 14476 Golm, GERB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         903
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1. 903
(Acquism="Arabidopsis thaliana" /mol type="genomic DNA" /morIety="Col"
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AJ243592.
AJ243592. GI:1458984
inositol-(1,4,5) trisphosphate 3-kinase.
Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
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RNGGRILMAYENESILANGGGDDAPERAQVKLVDFAHVLDGNGVIDHNFLGGLCSFIK
PIKDILQSVEKHDETDTSLLENGR"
                                                                                                                                                                                                                                                                                               Cheuk, R., Chen, H., Kim, C.J., Meyers, M.C., Banh, J., Bowser, L., Chenk, R., Chen, H., Kim, C.J., Meyers, M.C., Banh, J., Bowser, L., Carninci, P., Chang, E., Dale, J.M., Goldsmith, A.D., Hayashizaki, Y., Ishida, J., Jones, T., Kamiya, A., Karlin-Neumann, G., Kawai, J., Landa, J., Lan, J., Miranda, M., Narusaka, M., Nguyen, M., Onodera, C.S., Palm, C.J., Quach, H.L., Sakurai, T., Satou, M., Seki, M., Southwick, A., Tang, C.C., Toriumi, M., Wu, H.C., Yamada, K., Yang, C.C., Yamamura, Y., Yu, G., Yu, S., Shinozaki, K., Davis, R.W., Theologis, A.
Cheuk, R., Chen, H., Kim, C.J., Meyers, M.C., Banh, J., Bowser, L., Carninci, P., Chang, E., Dale, J.M., Goldsmith, A.D., Hayashizaki, Y., Eshida, J., Jones, T., Kamiya, A., Karlin-Neumann, G., Kawai, J., Lam, B., Lee, J.M., Lin, J., Miranda, M., Narusaka, M., Nguyen, M., Onodera, C.S., Palm, C.J., Quach, H.L., Sakurai, T., Satou, M., Seki, M., Yamamura, Y., Yu, G., Yoniuni, M., Wu, H.C., Yamada, K., and Ecker, J.R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Direct Submission
Submitted (08-JAN-2002) Salk Institute Genomic Analysis Laboratory
(SIGNAL), Plant Biology Laboratory, The Salk Institute for
Biological Studies, 10010 N. Torrey Pines Road, La Jolla, CA 92037,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RIKEN Genomic Sciences Center (GSC) members carried out the collection and clustering of RAFL cDNAS (RAFL cDNA: 'RIKEN arbidopsis Full-Length cDNA'): Seki,M., Narusaka,M., Ishida,J., Satou,M., Kamiya,A., Sakurai,T., Carninci,P., Kawai,J., Hayashizaki,Y. and Shinozaki,K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The Salk, Stanford, PGEC (SSP) Consortium members carried out the sequencing and annotation of the RAFL cDNAs: Cheuk, R., Chen, H., Kim, C.J., Meyers, M.C., Shinn, P., Banh, J. Bowser, L., Dale, J.M., Goldemith, A.D., Jiang, P.X., Jones, T., Karlin-Neumann, G., Lam, B., Lee, J.M., Lin, J., Liu, S.X., Miranda, M., Nguyen, M., Onodera, C.S., Palam, P.K., Quach, H.L., Southwick, A., Tang, C.C., Toriumi, M., Yamada, K., Yamamura, Y., Yu, G., Yu, S., Davis, R.W., Theologis, A., and Ecker, J.R.
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Location/Qualifiers
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/note="This clone is in
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /mol_type="mRNA"
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Unpublished
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and Ecker, J.R.
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JOURNAL
REFERENCE
AUTHORS
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JOURNAL
            AUTHORS
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Axabidopsis thaliana AT5g61760/mac9_60 mRNA, complete cds.
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Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Angnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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                                                                                                                                                                                                                                                                                                        180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            162 AlaMetAspThrAlaGlyValArgArgValLeuArgArgTyrValSer----SerVal 179
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         123 LysCysLeuAlaLysAspArgGlyThrThrSerValLeuLeuGlyPheArgValSerGly 142
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                                                                                                                                24 LeuIleAspGlySerGlyLeuPheTyrLysProLeuGlnAlaGlyAspArgGlyGluHis
                                                                                                                                                                                                                                                                                                                                                               64 Thr Phe Phe ProArg Phe His GlyThr Argieu Leu Pro Thr Gluala Gln Pro GlyGlu
               LeuHisProProGluHisGlnValAlaGlyHisArgAlaSerAlaSerLysLeuGlyPro
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                                                                                  44 GluvalAlaPheTyrGluAlaPheSerAlaHisAlaAlaValProAlaArglleArgAsp 63
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                                                  LeulleAspGlySerGlyLeuPheTyrLysProLeuGlnAlaGlyAspArgGlyGluHis 43
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               GlyAspGlyValIleAspHisAsnPheLeuGlyGlyLeuCysSerLeuIleLysPheVal
                                                                                                                                                                                                                           LysCysLeuAlaLysAspArgGlyThrThrSerValLeuLeuGlyPheArgValSerGly
US-10-042-894A-8 (1-289) x AY072621 (1-903)
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Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACCAD
clade, Panicoideae, Andropogoneae, 2ea.
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clade; Panicoideae; Andropogoneae; Zea.
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clade, Panicoideae, Andropogoneae, Zea.
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ADIKIGAIT"
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                                                                                                                                                                                      Length 899;
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1. .899
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89. .424
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       51.0%; Score 686; DB 6;
llarity 88.7%; Pred. No. 7.5e-98;
Conservative 0; Mismatches 40
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sativa (japonica cultivar-group)"

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codon_start=1
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                                                                                                                                                                      Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
          824 GGGGGCTCTGCTAGCTGATCAAGTTTGTTTCTGACATTGTTCCAGAGACTCCTTAGACG 883
GCCGCGCTCTGCTCGTTCAAGTTCGTTTCTGACATTCTTCCGGAGACTCCTCATACG 900
                                                                                                                                                                                                                                 Sasaki,T., Matsumoto,T. and Katayose,Y.
Oryza sativa nipponbare(GA3) genomic DNA, chromosome 2, BAC
clone:OSJNBa0047A17
                                                                                                                                                                                                                                                             Published Only in Database (2002)
2 (bases 1 to 149142)
Sasaki,T., Matsumoto,T. and Katayose,Y.
Direct Submission
                                                                                                                                                   AP005749.3 GI:49388911
                                        901 CAGC 904
                                                           CAGC 887
                                                           884
                                                                                                                                                   VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                      DEFINITION
                                                                                                                                                                                                                                                                        REFERENCE
AUTHORS
TITLE
JOURNAL
                                                                                                                                                                                                                                  AUTHORS
TITLE
                                                                                                                                           ACCESSION
                                                                                         RESULT 7
AP005749
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22880. .22936, 23369. .23417, 23504. .23652, 24724. .24771,
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complement(11599. .12180)
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/gene="OSJNBa0047A17.2"
/forte="Riesers = Lost = Lo
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/note="contains full-length cDNA(s): AK109226
non-coding transcript
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join (2637. 2780,3298. .3360)
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predicted by GENSCAN
this category is not in-
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192

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147160 TCCACCACCGCCGCCGCCGCCGCCGCCGCCATGGC--CTCCGACCTGCGCCCGCCG 147217
                                                           147278 GAGGGGTCTTCTACAAGCCCCTCCAGGCCGGGGAGCGGGGGGAGCACGAGGACGCCTTC
                                                                                                                    133 TCCGGCCTCTTCTACAAGCCGCTCCAGGCGCGCGACCGTGGGGAGCACGAGGTCGCCTTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4 ;
                                                                                                                                                                             /product="putative copine III"
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PFLLISRISESGVPVPICKTEVRKNDLNPKWKPVILNLQQIGSKENPLIIECFNFSSN
GKHDLIGKIVKSVAELEKMYHSQDGENFFVPASTAHDSHSKEVLKSQVYVEKYLENNR
                                                                                                                                                                                                                                                                                                                                                         QTFLDYISAGCQLNFMVAVDFTASNGNPRLPDSLHYIDPTGRPNAYQRALLEVGDVLO
YYDPAGRFPSWGFGARPIDGPVSHCFRUNGSTYGDFUGGIQGTMAAY ISALRWYSLAG
PTLFGPVVSTATALANQQXYFVLLIYTDGWTDFQFTIDAIIKASDPLSIL
VVGVGGADFKEMFELDPNKGERLESSTGRVASRDMIQPAPMKDAHGSGISTVQSLLAB
  Comptement (Join(19554. 19648,19740. 19836,20081. 20194, 20280. 2044,20690. 20827,20923. 20999,21093. 21207, 21277. 21382,21703. 21764,21859. 21893,22149. 22331, 22880. 22936,23369. 23471,23562.
                                                                                                                                                                                                                                                                                SWNARINVHYQFEVLQPIVFQVYDIDPQFHDVNEKMLKLEEQQFLGEAVCLLSEVITK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          oin(26913. .27610,27708. .29002,29099. .29157,29238.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13 TCCGTCACCCTCGCGCCCATAGTCCCCTTCCCCATACCATGTCCGACCTCCACCGCCG
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contains full-length cDNA(8): AK120851"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 149142;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         complement(26424. .26747)
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complement(join(<26424. .26494,26660. .>26747))
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fnote="Petart and end point are not identified"
for(30264. .30393,30451. .30605)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="start and end point are not identified" complement(join(26424. .26494,26660. .26747)) /gene="OSJNBa0047A17.7"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gene="OSJNBa0047A17.8"
oin(26913. .27610,27708. .29002,29099.
gene="OSJNBa0047A17.8"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     note="predicted by GeneMark.hmm etc."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 40.7%; Score 546.4; DB 8; Best Local Similarity 77.5%; Pred. No. 3.1e-76; Matches 718; Conservative 0; Mismatches 191;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 'note="predicted by GENSCAN etc."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          33031. .37214
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gene="OSJNBa0047A17.9"
                                                                                                                                                                                                                                                                                                                                                                                                                                           I PGQFMTYMRTREIQAIS"
                                                                                 25582. .25746))
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      CDS
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147998 TIGGCCGGCTCTGCTCGCTCATCATCGCCGACATTGTCGCCGAGGTTACCGAG 148057 147577 147637 147757 147817 147877 147937 147397 147457 147517 147697 897 PLN 29-JUN-2004 chromosome 2, 837 252 489 546 909 726 369 AAGGACCGCGAGCCACCACCACCCTCCTCGGCTTCCGCGTCTCCGGCGTCTCGGGTGTCT TACGCCGCGTTCACCGCGCACCCGGCCGTCCCGCCCCCGGGTCCGGGCGCCTTCTTCCCG 147638 GATGCCCGGGGGGGGCGCCGTGTGGCGCCCGGACCGGAGCTGAAGGGGATCGACGCC 147698 decededecededes de construcción de contra de cont CTGGGCGGGCTCTGCTCGATCAAGTTCGTTTCTGACATTGTTCCGGAGACTCCTCAT GCCGGCGTCCGCCGCGTGCTCCGGCGCTACCGTTGCCGACGACGATGGAC TGTGCGCTCCCCCCCCCGCGTGTACGGAGAAAGGTGGAGTCTTGTCACAGCTGCGCGAG CTCAAGGCGTGGTTCGAGGAGCAGCAGTTCTTCCACTTCTACTCGGCGTCGATTCTTCTG GGCT-----ATGATGCTGCTGCAGTCGCAGCAGCCGGAGATGGGGGTGGGGTGACG 147878 GECTACGACGCCAATGCGGCGGCGGCGGCTGCTCCCGGAGGTGGAAGCGGCGGTGTAAGG GTGAAGCTGGTGGACTTTGCCCCATGTGGCGGTGATGGGGTGATTGACCACAACTTC TATGAGGCGTTCTCCGCCCACGCCGCCGTCCCGGCCCCGCATCCGAGACACCTTCTTCCCC CGGTTCCACGGCACGCGACTCCTCCCCACCGAGGCGCAGCC---CGGGGAGCCGCATCCT CACCTCGTCCTCGACGACCTCCTCGCGGGGTTTCAGGCGCCCTGCGTCGCAGACATCAAG 370 ATCGGCGCATCACGTGGCCACCGAGTTCGCGGGAGCCCTACATCGCCAAGTGCGTCGCC AAGGACCGCGGGACCACGAGCGTTCTGCTCGGATTCCGCGTCTCCGGCGTCCGAGTCGTC --- GGCCCCGAGGCGCCGTGTGGCGGACGGAGCCCCGGAGGTGAAGGCCATGGACACC linear genomic DNA, 157419 bp DNA Oryza sativa (japonica cultivar-group) PAC clone:P0415B12. Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group) AAGGCGTCTTCAGATCATTCTTGAAA 148083 ACGCAGCCTTTGGGTCCTTCTTAAGA 923 VERSION KEYWORDS SOURCE ORGANISM

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TOWNERS TO STANDARD THEORY OF THE STANDARD TO STANDARD TO STANDARD TO STANDARD TO STANDARD THEORY OF THE STANDARD TO STANDARD TO STANDARD THEORY OF THE STANDARD THEORY OF THE STANDARD THEORY OF THE STANDARD THE ST
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SULTSSTYTTGTAANSEGKTAMVAATVCSMKGSLEKGPTNPRVTREHVVGSRGLCRL
roomplement (8669. 15038)
/gene="P0415B12.3"
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KQVELFVGRVRSCGHGTPTLSAFASSVDSWLMRLKRAALKEEEQLFLSVERTITLLGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                // Joce="supported by full-length cDNA(8): AK065061"

complement (join(16881. .17069,17267. .17644,18400. .18594,

18674. .18151,18816. .19001,19077. .19307,19386. .19739,

19837. .20034,20118. .20288,20405. .20512,20611. .20829,

20914. .21120,21227. .21445,21564. .21638,21998. .22150))
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            complement (join(8929. .9060,9161. .9334,9438. .9569,
9640. .9738,9929. .10000,10080. .10136,10206. .10379,
10460. .10554,10727. .10826,10921. .11073,11145. .12275,
12870. .12980,13078. .13240,13613. .13707,13793. .14053,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                complement (join(8669. .9060,9161. .9334,9438. .9569,
9640. .9738,9929. .10000,10080. .10136,10206. .10379,
10460. .10554,10727. .10826,10921. .11073,11145. .12275,
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/note="supported by full-length cDNA(8): AK121782"
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contains full-length cDNA(s): AK121782"
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join(6055. .6067,6850. .7404)
note="Pol515112.2"
/note="predicted by FGENESH etc."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /product="RNA binding protein Rp120"
/protein_id="BAD25376.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'note="contains EST(s):
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/gene="P0415B12.4"
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                                                                                     SOS
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                                                                                                                                                                                                                                                                                                                                                                 Saaaki,T., Matsumoto,T. and Yamamoto,K.
Direct Submission

2-1-7 TSHUMDA. TBATAKI 30-9-860; Japan

2-1-7 TSHUMDA. TBATAKI 30-9-860; Japan

(E-mail:teasakienias affrc.go.jp, URLihttp://rgp.dna.affrc.go.jp/,
Tel:g1-298-38-7441, Fax:B1-298-38-744168)
On Jun 28, 2004 this gequence version replaced gi37437094.
Genes were predicted from the integrated results of the following:
GENSCAN (http://com/loinitie.com/). GeneMark. hum
(http://www.icjr.org/lointermern/glum.frcm.html), FGENESH
(http://www.icjr.org/lointermern/glum.frcm.html), RiceHWM
(http://www.icjr.org/lointermern/glum.frcm.html), gap2
(http://www.icjr.org/soitwern/glum.min.go.jp/min.html), gap2
(http://www.icjr.org/soitwars/glimmern/glum.html), gap2
(http://www.icjr.org/soitwars/glimmern/glum.html)

BLASTN with identity or significant homology to a protein in gcluseded as a protein of gcluselificant homology to any protein but with genemer gene prediction programs is probable whypothetical protein acc
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae,
Ehrhartoideae, Oryzeae, Oryza.
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mol type="genomic DNA"
cultivar="Nipponbare"
                                                                                                                                                                     Sasaki,T., Matsumoto,T. and Yamamoto,K.
Oryza sativa nipponbare(GA3) genomic DNA, chromosome 2, PAC
clone:P0415B12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             probably inactive due to including stop codon(s) probably inactive due to too long 3'UTR in CDS"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                complement (4313. .5807)
//gene="P0415B12.1"
//ce="conteains full-length cDNA(s): AK121467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /gene="P0415B12.2"
join(<6065. .6067,6850. .>7404)
                                                                                                                                                                                                                                                                                                       Published Only in Database (2002)
2 (bases 1 to 157419)
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/gene="P0415B12.1"
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The Rice Full-Length cDNA Consortium, National Institute of Agrobiological Sciences Rice Full-Length cDNA Project Team:, Kikuchi, S., Satch, K., Nagata, T., Kawagashira, N., Doi, K., Kikuchi, S., Satch, Y., Nagata, T., Kawagashira, N., Doi, K., Kikuchi, S., Satch, J., Ishikawa, M., Yamada, H., Ooka, H., Hotta, I., Kojima, K., Namiki, T., Chneda, E., Yahagi, W., Suzuki, K., Li, C., Ohtsuki, K., Shishiki, T., Foundarion of Advancement of International Science Genome Sequencing & Analysis Group:, Otomo, Y., Murakami, K., Iida, Y., Sugano, S., Fujimura, T., Suzuki, Y., Tsunoda, Y., Murakami, K., Ishibiki, J., Masuda, H., Kobayashi, M., Xie, Q., Lu, M., Narikawa, R., Sugiyama, A., Mizuno, K., Yoshimura, A., Mitura, J., Kusumegi, T., Oka, M., Ryu, R., Ueda, M., Matsubara, K., Riken; Kawai, J., Carninci, P., Adachi, J., Aizawa, K., Arakawa, T., Fukuda, S., Hara, A., Hashidume, W., Hayatsu, M., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kondo, S., Konno, H., Miyazaki, A., Osato, N., Ota, Y., Saito, R., Shinagawa, A., Shiraki, T.,
10186 CACATCGTCCTCGACGACCTCCTCGCGGGCCTCCCGTCCCCCTGCGTCGCCGACGTCAAG 40245
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Oryza sativa (japonica cultivar-group) cDNA clone:J023018G11, full
insert sequence.
AK072296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AK072296.1 GI:32982319
FLI_CDNA; CAP trapper.
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopaida; Poales; Poaceae;
                                                                             10366 GATGCCCGGGGCGCCCCGTGTGGCCCCGGACCGGTCGGAGCTGAAGGGGATCGACGCC
                                                                                                                                                                                                                                                                                                                                                                                                           40606 GGCTACGACGCCAATGCGGCGGCGGCGGCTGCTCCCGGAGGTGGAAGCGGCGGTGTAAAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            838 CTGGGCGGGCTCTGCTCGCTGAICAAGTTCGTTTCTGACATTGTTCCGGAGACTCCTCAT
                                                                                                                                                                                                                                                               ---GGCCCCGAGGGCGCCGTGTGGCGGACGGAGGCCCCGGAGGTGAAGGCCATGGACACC
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                                                                                                                                                                                                                                                                                                                                                                GCCGGCGTCCGCCGTGCTCCGGCGCTACGTGTCATCCGTTGCCGACGAGGGGATGGAC
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                     /translation="MASATGASGWLRGKVKGVTSGDCLLIMGSTKADVPPPEKSITLS.
YLMAPRLARGGVDEPPAWESRETLERKLCIGKEVTFRVDYTAPNVGREFGTVYLGDKGVAYSITAAGWARVEGGPFGGEPSPYLLGKKLCIGKEVTFRVDYTAPNVGREFGTVYLGDKGVAYSITAAGWARVEGGPAAEESIRD
LPPSAJGEASGFDAKGFAVANKGKSLEAIVEGVRDGSTVRYLLLPSFOFFVQITVAGVO
SPSMGRRPPPRTVLMRDVAIVVEGTDSFSNIIGSYYSDGGTLKADLALELVENGLAKYVE
WSAMMMDVDAKIKLKNABLQAKVDGLTNTGFRPPYTNSKPIHDQKTTGKVVEVVSGD
CIIVADDAAPYGSPSARRVNLSSIRAFWGNDRFRDEKFDNTRKFLIGKO
VTVEMBYSRRISTVDGGPTTNTADARVLDSFRODNGSIPSGGDVGGT
                                                                                                                                                                                                                                                          NIAETLLSRGFARTSKHRDYEERSHYPDLLLAAESRAEKAKKGVHSAKESPVMHTDD.
TTVSAKKARDPLPFLQRNRRHSALVEYVFSGHRPKLTIPKETCSIAFSFSGVRCPGKD
EPYSNBALALMRRRILQRDVBIEVBAVDRTGTFLGSLWESKTNMASVLLEAGLAKLSS
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                                                                                                                                                                                                                                                                                                                                     FGLDR I PDANVLMRAEQSAKQQKLKIWENYVEGEEVSNGSASESKQKEI LLKVVVTEVL
GGGKFYVQTVCOHRVASI QQQLASLKLKDAPVI GAFNPYWGEI VLAQFSADNSWNRAM
I VNGERGAVSGODKFEVFY I DYGQDVVPY SRI READPSI SSSPALAQLGSLAFIKV
PNLEDPFGHEAAVYLNDCLLNSQKQYRAMI BERDTSGGKSKGQGTGI LI VTLVDAET
                                                                                                                                                                                                                                                                                                                                                                                                                                              ETSINATMLEEGLARLERSKRWDTRERKAALQNLEQFQEKAKKERLQIWQYGDVESDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      note="probably inactive due to including frameshift(s) in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    192
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /gene="P0415B12.7"
/note="similar to Oryza sativa chromosome7, P0404G11.101"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CGGTTCCACGCACGCGACTCCTCCCCACCGAGGCGCAGCC---CGGGGAGCCGCATCCT 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CACCTCGTCCTCGACGACCTCCTCGCGGGGTTTCAGGCGCCCTGCGTCGCAGACATCAAG 369
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         probably inactive due to including stop codon(s) in CDS pseudogene, TNP2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GAGCACCAAGTCGCCGGCCACCGCGCCTCCGCCAGCAAGCTGGGCCCGCTCATCGACGGC
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this category is not included in IRGSP standard"
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/gene="P0415B12.7"
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Pred. No. 3.1e-76;
0; Mismatches 191; Indels
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gene="p0415812.5"

join(25322. .25357,28498. .28641)

gene="p0415812.5"

/note="hypothetical ORF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /product="hypothetical protein"
/protein_id="BAD25377.1"
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/gene="P0415B12.6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gene="P0415B12.6"
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Best Local Similarity 77.5
Matches 718; Conservative
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PUBMED REFERENCE AUTHORS

MEDLINE JOURNAL

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                                                                                                                                                                   TAIGAGGCGIICICCGGCCGAGGCCGCCGGCCGGCAICCGAGACACCIICIICCCC 252
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      430 AAGAACCGCGGGACCACGAGCGTTCTGCTCGGATTCCGCGTCCGGGGTCCGAGTCGTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATCGGCGCCATCACGTGGCCACCGAGTTCGCCGGAGCCCTACATCGCCAAGTGCCTCGCC
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                                                                                                                                                                                                                                                         GAGCACCAAGTCGCCGGCCACCGCGCTTCGCCAGCTGGGCCCCGCTCATCGACGGC
                                                                                 TCCGTCACCCCTCGCGCCCATAGTCCCCTTCCCCATACCATGTCCGACCTCCACCCCGCCG
        Mismatches 192; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pals Genome Sequencing & Analysis Group: Otomo, Y., Iida, Y., Fulimura, T., Ikeda, R., Ishibiki, J., Kawamata, M., Kobayashi, M., Kodayama, T., Kusumegi, T., Lu, M., Masuda, H., Miura, J., Mizuno, K., Narikawa, R., Nikura, J., Oka, M., Ryu, R., Sugano, S., Sugiyama, A., Suzuki, Y., Tsunoda, Y., Ueda, M., Kie, Q., Yokomizo, S., Yoshimura, A., Matsubara, K. and Murakami, K. Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in Riken: Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Carninoi, P., Fukuda, S., Hangaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hori, F., Iida, J., Imamura, K., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kanagawa, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matcuyama, T., Miyazaki, A., Murata, M., Nashi, K., Nomura, K., Nimasaki, R., Ohno, M., Osato, N., Ota, Y., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Sato, K., Shibata, K., Shihagawa, A., Shiraki, T., Sasaki, D., Sato, K., Shibata, K., Shikata, K., Shikat
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NIAS Rice Full-Length cDNA Project Team: Kikuchi,S., Satoh,K.,
Nagatat,T., Kawagashira,N., Doi,K., Kishimoto,N., Yazaki,J.,
Ishikawa,M., Yamada,H., Ooka,H., Hotta,I., Kojima,K., Namiki,T.,
Ohneda,E., Yahagi,W., Suzuki,K., Li,C., Ohtsuki,K., Shishiki,T. and
Yamamoto,M.
                                                   over 28,000 cDNA clones from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Direct Submission
Submitted (05-DEC-2001) Shoshi Kikuchi, National Institute of
Agrobiological Sciences, Department of Molecular Genetics, Head of
Laboratory of Gene Expression; 2-1-2 Kannondai, Tsukuba, Ibaraki
305-6602, Japan (E-mail:skikuchi@nias.affrc.go.jp,
Tel:81-29-838-7007, Fax:81-29-838-7007)
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Pred. No. 9e-76;
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                                               Collection, mapping, and annotation japonica rice
                                                                                                                                     ence 301 (5631), 376-379 (2003)
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/cultivar="Nipponbare"
/db_xref="taxon:39947"
/clone="J023018G11"
                 (oshino, M. and Hayashizaki, Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        40.5%;
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Best Local Similarity
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TITLE JOURNAL

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KEYWORDS SOURCE ORGANISM

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Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACCAD
clade, Panicoldeae, Andropogoneae, Zea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        182 CGAGGGTGATGGGGTGATTGACCACAACTTCCTGGGGGGGCTCTGCTANCTGATCAAGTT
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Novel inositol polyphosphate kinase genes and uses thereof
Patent: WO 02059324-A 18 01-AUG-2002;
PIONEER HI-BRED INTERNATIONAL, INC. (US)
                                                                                                                                                                                                                                                                                                                                                                                                                                         1;
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Pred. No. 2.1e-20;
0; Mismatches 21; Indels 5
                                                                                                                                                                                                                                                                                                                                                                 Length 519;
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                                                                                                                                                                                                                                                                                                                                                                 Score 298.4; DB 6;
Pred. No. 3.8e-37;
0; Mismatches 38;
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/mol_type="unassigned DNA"
/db_xref="taxon:4577"
                                                                                                                                                                                                                          DNA.
                                                                                                                                                  1. .519
/organism="Zea mays"
/mol_type="unassigned
/db_xref="taxon:4577"
                                                                                                                Location/Qualifiers
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al Similarity 90.2%;
238; Conservative (
                                                                                                                                                                                                                                                                                                                                                             Query Match
22.2%;
Best Local Similarity 89.4%;
Matches 328; Conservative
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Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACCAD
clade, Panicoideae, Andropogoneae, Zea.
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Shi,J., Beach,L.R., Wang,H., Rafalski,J.A. and Cahoon,R.E. Novel inosicol polyphosphate kinase genes and uses thereof Patent: WO 02059324-A 17 01-AUG-2002;
PIONEER HI-BRED INTERNATIONAL, INC. (US)
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Submitted (22-MAR-2001) Dodds P.N., Plant Industry, CSIRO, GPO 1600, Canberra, ACT 2601, Australia
1600, Canberra, ACT 2601, Australia
1. .25054
                       GGGAGCCGCATCCTCACCTCGTCCTCGACGACCTCCTCGCGGGGGTTTCAGGCGCCCTGCG
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                                                                                                                                                                                                                                                                                                                                 GCGTCCGAGTCGTCGGC----CCCCGAGGGCGCCCGTGTGGCGGACGGAGCGCCCGGAGGTGA
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Contrasting modes of evolution acting on the complex N locus rust resistance in flax
Plant J. 27 (5), 439-453 (2001)
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Spermatophyta, Magnoliophyta, eudicotyledons, core eu
rosids, eurosids I; Malpighiales, Linaceae, Linum.
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AJ310150.1 GI:13509206
10gc-A gene; Ngc-A protein; N
Ngc-D protein:
Linum usitatissimum (flax)
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/protein id="CAD52956.1"
/protein id="CAD52956.1"
/db_xref="G1:21359675"
/tanslation="MLKVPDHQWGHRGDGGKLGPLVDDSGRFYKPLQSDHRGDTEVA
/translation="MLKVPPAHGTKTIEASDGSGPQPHLVLBDLVSGRTNPSLANDIK
FYESFYSNTEI PGHIRKFPARHGTKTIEASDGSGPQPHLVLBDLVSGRTNPSLANDIK
TGSRTWYPEASEEXIQKCLEKDRNSTSVSLGFRISGLRVYQNSEAGFWQPEKKVVYSF
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PYSCSLIILYDRESALDGCAHPKVKLVDFAHVMDGHGVIDHNPLGGLCSVIKFIRDIA
DEDNKCAKCEVNLGLKENGFYKSSTEPELDHEAC"
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Eucalyptus grandis
Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; Myrtales; Myrtaceae; Eucalyptus.
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                                                                                         GGCTATGATGCTGCTGCAGTCGCANCAGGCGGAGGTGGGGGTGAGCGGTAACAGTGAAGGTG 120
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                                                                                                                                                                                CCATGCTCAAGGTCCCGGATCATCAAGTCGCCGGTCACCGGGGAGACGGGGAAAGCTGG 173
                                                                                                                                                                                                                                                       GGCTCTGCTCGCTGATCAGTTC--GTTTCTGACATTGTTCCGGAGACTCCTCATACG-C 901
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                                                  GCCTATGATGCTGCTGCAGTCGCAGCAGCGGGAGATGGGGGGTGGGGTGAAGCTG
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'note="unnamed protein product"

    .1195
    ^organis="Eucalyptus grandis"
    fmol type="unassigned DNA"
    /db_xref="taxon:71139"

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/gene="Ngc-A"
join(12668. 13218,13450. 14542,14757. 15032,15186. 16493)
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ONLTADEVRLVLKRFVSSNPKSDQPDCSFAAVVYGGSNGI LAQLLELKAWFEDQTI YH
FNSCSVLMLYEKEKTKMVNGGEESLGCAAVKLI DFAHVTEGNGVI DHNPLGGLCSLI K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DEVVGLINLDSSTSEKI IGIHGMGGLGKTTLAKAVYDKVSTKFERCYFLENIRDTLSB
KNGYSILQNKI ISGTLRKDFNEAKNASDGIR I IR DRVCRHKLLIVLDDVDEKFGFDDV
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DYALLSKEFVQAAGLELYIKVIGSLLFRMDKI FWERELLEFFKKI SPTKVQERKLKISY
NELTHNEKQI FLDIACYFIGSQKI YPI FWWEDCDFYPESTIRSLIQRSLIKLORSRIK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GDVLNTFWMHDHIDLGRAIVREEKNONPYKRSRIWSNKDAVNMLKHKKGTDČVEVLT
VDMGESBLILTNKREFEKLTMAKYLKOSNRALADDFKDVLDANDRALLESSCDSVPSGLY
LKKLVRLDLHOCOSDSWKGNNELKVARKLKAVSLKRCFHLKKVPDFSDCGDLEFELNF
DGCRNNRGEVDIGNFKSLRFLYISKTKITKIKGEIGRLIANLKYLSVGDSSLKEVPAGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SKLSSLEFLALALTDSYKSDFTEMLFTSLTLLYISNDTQKFCPDTSSENLQRLPNLSN
TINESVLYLIDVGGETGGELGALENESTLSIGARSRIVHIDGEBULVLDHLRYBEGR
ILRKLPSLJALTRLQUCPLWIGOCPLVTEINGMGQLWESLSHLKVVGCSALIGLSSLHSN
VKLERLLLVGCVLTETWPPSLSMFTKLTELSLCAMPWKQFPDLSNLKNLRVLCMSFCQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FYTSFSAHKTI POHVRRFFPAFHGTQSIBASDGSGLHPHLILEDLTSTRLHPCVMDIK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LQELAKAVGCWKSGGGAKGQHIILPVFLFVDPRDVRHTESGSYKEAFEEHSQKHDPET
VLEWKEALQEVGEMKGYHVTESDGHGSIIDKILTEVELHLGANYALVTDELVGIDSRV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SLEELKWSGCESTEELPNLSGLKNLRELLLKGCTQLKEVNGLEGLELTVFEARKRIKA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /tränblation="mmksdsngstdsfhscssadltfppllpsgeyevflsfrgpdvrk
Tfadhlytslvrskfrtfrdeeellekggtigpsliraiteskiyipiltpnyasskwc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ELIEVPGLDALESLKWLSMEGCRSIRKVPDLSGLKKLKTLDVESCIQLKEVRGLERLE
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/note="SiTe of 11 bp insertion in n-X50 rust susceptible
mutant allele"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /standard name="n-X128A"
/note="Site of LUTE transposon insertion in n-X128A rust
susceptible mutant allele"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /evidence=experimental
3397. .6629
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/note=233 bp deletion in n-X139 rust susceptible mutant
                                                                                                                                 join(2881. .3431,3533. .4652,4770. .5045,5140. .6519)
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                                                                                                                                                                                                                      join(2881. .3431,3533. .4652,4770. .5045,5140. .6519)
gene="Ngc-D"
                                                                                                                                                                                                                                                                                                       note="N rust resistance gene: TIR-NBS-LRR protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    related to human inositol hexakisphosphate kinase
protein"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FISEILTGPDENSPKSCLQDGAAE"
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db_xref="GI:13509207"
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variety="Bombay"
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                                                                                              'db_xref="taxon:4006"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      codon_start=1
                                                                                                                                                                                                                                                                                                                                             codon start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gene="Ngc-D"
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gene

SOS

CDS

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join(20265. .20815,21104. .22202,22415. .22690,22818. .24218)
|gene="Ngc-B"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /db_xref="Uniprot/Tremal.09aRC1"
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FNSCSVLMLYEKEKTKWVNGGEESLGGAAVKLIDFAHVTEGNGVIDHNFLGGLCSLIK
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FGKLGDFSTDSRFLITTRDARTLELLNECKMFGLEEMSHDHSLQLFSKHAFGVDYPPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DEMVKLINLDSTSEKTIGIYGMGRLGKTTLATAVYNKVSMQFERCCFLDNIRETLLKN
DEMVKLINLDSTSEKTIGIYGMRABOOVQMTREREVSHKIFTVVLDDVNBSFREDDIF
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ITNBERFKQFSRLRFLEVLNGDLSGNFWVVLPSLRWLRVYHGDPCPSGLNLNKLEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /translation="MMRSDTDSSIGFLSRSSVDPTLPLLPSGEXBVFLSFRGPDVRQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DYASLCEEFIQVASGLPLALKVIGSILFKSDKRFWEDKLIELKAIPSAKVQERLKVSY
NELTHNEKQIFLDIACLFVGAKKEVPMYMWSDCDLYPASTLRTLVQKSLVRMDDNKKF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ELDGCYVTHSWKGWNEIKAAGKLKVVNLTSCGILEKVPDLSTCRGLELLCFHKCQWMR
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LTRLHLKEVGIHEIPGGLGKLKLLESLSICNPNLDNLDGLENLVLKELALERCPILG
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ILEWKGALQFGKWKGWHISELTGQGAVVDKIFTEVELHLRANYTLATDELVGIDFSV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EVSDVTDSWEGWNEIKAAGKLKVVHLMCCKGLEKVPDLSTCRGLELLRFSICRRMIGE
LIDINKFOLDSTLEVTRITPLKGEVRSLQNLQQDVOKSSGLIEVPAGEISKLSSLEXT
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RLRLEEVGIHGIPGLGELKLLECLFIRDAPNLDNLDGLENLVLLKELAVERCRILEKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PSLAELTKLHKLVIGQCNILGEIYGLANLGESLSHLEISGCPCLTVVESLHSLLNLGT
ELEGSYGTIYNLPPSLSIYTKLKSLKVSDSQLDEDLTNLKNKTCLKIGGCDNFIETTGL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          related to human inositol hexakisphosphate kinase 2
rust resistance gene homolog: TIR-NBS-LRR
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protein_id="CAC35325.1"
db_xref="GI:13509211"
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                                          protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    orotein"
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TGGCCGAGGGTGATGGGGTGATTGACCACATTCCTGGGCGGGGCTCTGCTGGTCA 862
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SRKGKQLVTQSARRALFINN"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9898
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                                   603 GAGGCTTGCAGAAGCTCAAGGACTGGTTCGAGGTTCAGACGTGTATCACTTCTATTCT 662
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Searched:

Database

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US-10-042-894A-7

US-10-042-894A-7

Sequence 7, Application US/10042894A

Publication No. US2003009011A1

APPLICANT: Beach, Larry

APPLICANT: Rafalski, Antoni J.

PRESTICANT: Rafalski, Antoni J.

APPLICANT: Rafalski, Antoni J.

PRESTICANT: Rafalski, Antoni J.

PRESTICANT: Rafalski, Antoni J.

PRESTICANT: Rafalski, Antoni J.

PRIOR REFERENCE: 128

PRIOR APPLICATION NUMBER: US 60/261,465

PRIOR PLING DATE: 2001-012

NUMBER OF SEQ ID NOS: 37

SOFTWARE: PastSEQ for Windows Version 4.0

SEQ ID NO 7

LENGTH: 1344
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                                                                                                                                                                                    June 17, 2005, 00:32:13; Search time 879 Seconds (without alignments) 9491.401 Million cell updates/sec
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Score

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Sequence 15, Appl Sequence 1, Appli

1091 CCTTTTTCCCAACCCTTACTTCCCAAGAACTTTTTTTTTCCACTTTGGGGGTTCCA 1140 1091 CCTTTTTTCCCAACCCCTTACTTCCGAAGAACTTTTTTTT	136 CGCCGGAGCACCAAGCCGCCGCCCCCCCCGCCAGCAAGCTGGCCCCCTCATCG 128 ACGCCTCCGGCCTCTTCTACAAGCCGCCCCCCCGCCGCCGCCGCCCCCCCC
Matches 1344; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Gacadastrastrocarcaccoccustrastrocarcaccascoccustrastrocarcaccascoccus 1 Gacadastrastrocarcaccascoccustrastrocarcaccascoccus 1 Gacadastrastrocarcaccascoccus 1 Gacadastrastrocarcacascoccus 1 Gacadastrastrocarcacascoccus 1 Gacadastrastrocarcacascoccus 1 Gacadastrastrocarcacaccascoccus 1 Gacadastrastrocarcacaccascoccus 1 Gacadastrastrastrastrocarcacaccaccaccaccaccaccaccaccaccaccacca	OP 781 AAGCTGGTGGACTTTGCCCATGTGGCCGAGGTGATTGACCACAACTTCCTG 840 Db 781 AAGCTGGTGGACTTTGCCCATGTGGCGGGGTGATTGACCACACTTCCTG 840 OP 841 GGCGGGCTTTGCCCATGTGGCGTGATGGGGTGATTGACCACACTTCCTG 840 OP 841 GGCGGGTCTGCTCGCTGATCGTTTCTGACATTGTTCCGGAGACTCCTCATACG 900 OP 901 CAGCCTTTGGTCGTCTGATTCTGACATTGTTCCGGAGACTCCTCATACG 900 OP 901 CAGCCTTTGGGTCCTTCTTAAGAGGGATCCTGGCATTTTCGATTTGATAACAAAGCCCTA 960 OP 901 CAGCCTTTGGGTCCTTCTTAAGAGGGATCCTGGCATTTTCGATTTGATAACAAAGCCCTA 960 OP 901 CAGCCTTTGGGTCCTTCTTAAGAGGGATCCTGGCATTTTGATTAACAAAAGCCCTA 960 OP 901 CAGCCTTTGGATCTTCTTAAGAGGGCTCCTGGCATTTTGATTTGATAACAAAAGCCCTA 960 OP 901 CAGCCTTTGGATCTTGTTGTTGATTGATAACAAAAGCCCTA 960 OP 901 CAGCCTTTGGATAAAAAAAAAAAAAAAAAAAAAAAAAAA

GENERAL INFORMATION: APPLICANT: Shi, Jinrui APPLICANT: Beach, Larry APPLICANT: Rafalski, Antoni APPLICANT: Rafalski, Antoni APPLICANT: Rafalski, Antoni APPLICANT: Rafalski, Antoni TITLE OF INVENTION: Genee and Uses Thereof CURRENT FILING DATE: 2002-01-09 PRIOR FILING DATE: 2001-01-12 NUMBER OF SEQ ID NOS: 37 SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 5 LENGTH: 923 TYPE: DNA ORGANISM: Zea mays FRATURE: MAME/KEY: CDS MAME/KEY: CDS MAME/KEY: CDS US-10-042-894A-5 US-10-042-894A-5	Query Match 64.4%; Score 865.4; DB 14; Length 923; Best Local Similarity 98.8%; Pred. No. 2.8e-236; Matches 870; Conservative 0; Mismatches 11; Indels 0; Gaps 0	Qy 42 TCCCCATACCATGTCCGACCTCCACCCGCGGGGGCACCAGCGGCCACCGGCGCCTC 101	Qy 102 CGCCAGCAAGCTGGGCCCCTCATCGACCGCTCCTTCTACAAGCCGCTCCAGGC 161	Qy 162 CGGCGACCGTGGGGAGCACGAGGTCGCCTTCTATGAGGCGTTCTCCGCCCACGCCGCCGT 221	Ay 222 CCCGGCCCGCATCCGAGACACTTCTTCCCCCGGTTCCACGGCACGCAC	Qy 282 CGAGGCGCGGGGAGCCGCATCCTCACCTCGTCCTCGACCACCTCCTCGCGGGGTT 341	Qy 342 TCAGGCGCCTGCGTGGCAGACATCAAGATCGGGGCCATCACGTGGCCCACCGAGTTCGCC 401	Qy 402 GGAGCCTACATCGCCAAGTGCCTCGCCAAGGACCGCGGGACCACGAGCGTTCTGCTCGG 461	Qy 462 ATTCCGCGTCTCCGGCGTCCGAGGGCCCCGAGGGGCGCCGTGTGGCGGACGGA	Oy 522 CCCGGAGGTGAAGGCCATGGACACCGCGGGGTCCGCGGTCCGGCGTCCGGCGTCCGGCGTACGTGTC 581 Db 523 CCCGGAGGTGAAGGCCATGGACACCGCCGGCGTCCGCCGCGTGCTCCGGCGTTCGGCGCTTCGGCGTTCGGCGTTCGGCGTTCGGCGTTCGGCGTTCGGCGTTCGGCGTTCGGCGTTCGGCGCTTCGGCGG	QY 582 ATCCGTTGCCGACGAGGGATGGACTGTGCGCTCGCCGCGGGGGTGTACGGAAAAGG 641 Db 583 ATCCGTTGCCGACGATGGACTGTGCGCTCGCCGCGGGGGTGTACGGAGGAAAAGG 642	642	
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Sequence 3, Application US/10042894A
; Sequence 3, Application US/10042894A
; Publication No. US20030009011A1
; GENERAL INFORMATION:
; APPLICANT: Shi, Jinrui
; APPLICANT: Rafalski, Antoni J.
; APPLICANT: Rafalski, Antoni J.
; APPLICANT: Rafalski, Antoni J.
; APPLICANT: Reacas E.
; TITLE OF INVENTION: Genes and Uses Thereof
; TITLE OF INVENTION: Genes and Uses Thereof
; FILE REFERENCE: 1286
; CURRENT APPLICATION NUMBER: US/10/042,894A
; CURRENT ELLING DATE: 2002-01-09
; PRIOR APPLICATION NUMBER: US 60/261,465
; RRIOR FILING DATE: 2001-01-12
; NUMBER OF SEQ ID NOS: 37
; SEQ ID NOS: 37
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62.3%; Score 837.4; DB 14; Length
Best Local Similarity 97.5%; Pred. No. 2.7e-228;
Matches 859; Conservative 0; Mismatches 21; Indels
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; LOCATION: (53)...(736)
US-10-042-894A-3
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ORGANISM: Zea mays
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US-10-042-894A-3
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Publication No. US20030009011A1

GENERAL INFORMATION:

APPLICANT: Beach, Larry

APPLICANT: Beach, Larry

APPLICANT: Rafalski, Antoni J.

APPLICANT: Rafalski, Antoni J.

APPLICANT: Rafalski, Antoni J.

TITLE OF INVENTION: No. US20030009011A1e1 Inositol Polyphosphate Kinase

TITLE OF INVENTION: Genes and Uses Thereof

TITLE OF INVENTION: Genes and Uses Thereof

TITLE OF INVENTION: Qenes Thereof
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                                                                                                                                                                                                        GATTGACCACAACTTCCTGGGCGGCTCTGCTCGCTGATCAAGTTCGTTTCTGACATTGT
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62.9%; Score 844.8; DB 14; Length 1169;
Best Local Similarity 97.2%; Pred. No. 2.2e-230;
Matches 890; Conservative 0; Mismatches 22; Indels 4;
                                                                                                                                                                                                                                                                                                                  NAME/KEY: CDS
LOCATION: (84)...(806)
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ORGANISM: Zea mays
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            382 ACATCAAGATCGGTGCCATCACGT------
CURRENT APPLICATION NUMBER: US/10/042,894A
CURRENT FILING DATE: 2002-01-09
PRIOR APPLICATION NUMBER: US 60/261,465
PRIOR FILING DATE: 2001-01-12
NUMBER OF SEQ ID NOS: 37
SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 20
LENGTH: 3416
                                                                                                                                                                                                                    Best Local Similarity 90.2
Matches 862; Conservative
                                                                                                                                                             ... (407)
                                                                                                          TYPE: DNA
ORGANISM: Zea mays
FEATURE:
                                                                                                                                                  ; NAME/KEY: CDS
; LOCATION: (72)
US-10-042-894A-20
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Sequence 20, Application US/10042894A

Publication No. US20030009011A1

GENERAL INFORMATION:

APPLICANT: Seach, Larry

APPLICANT: Rafalski, Antoni J.

APPLICANT: Rafalski, Antoni J.

TITLE OF INVENTION: No. US2003009011A1e1 Inositol Polyphosphate Kinase
TITLE OF INVENTION: Genes and Uses Thereof

FILE REFERENCE: 1286
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 TCTACAAGCCGCTCCAGGC
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US-10-042-894A-20
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TCGGTCAGAGGTTGTAAGCATGGAGGGAGCGTGTTGATCCGGCAACTGTGTCAGTCTTT 1225
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APPLICANT: Shi, Jinrui
APPLICANT: Beach, Larry
APPLICANT: Beach, Larry
APPLICANT: Rafalski, Antoni J.
APPLICANT: Rafalski, Antoni J.
APPLICANT: Cahoon, Rebecca E.
TITLE OF INVENTION: No. US2003009011A1e1 Inositol Polyphosphate Kinase
TITLE OF INVENTION: Genes and Uses Thereof
FILE REFERENCE: 1286
CURRENT APPLICATION NUMBER: US/10/042,894A
CURRENT FILING DATE: 2002-01-09
FRIOR APPLICATION NUMBER: US 60/261,465
FRIOR PILING DATE: 2001-01-12
NUMBER OF SEQ ID NOS: 37
SOFTWARE: FastSEQ for Windows Version 4.0
SSEQ ID NO 15
                                                                                                                                                                                                                             676 TCGGTCAGAGGTTGTAAGCATGGATGGAGGCGTGTTGATCCGGCAACTGTGTCAGTCTTT 735
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                                             617 GAAGAAAC-TTTTTTTTCCCACTTTGGGGGTTCGATTACGTTGGATCTGGTTTGTGCCAC
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Pred. No. 4e-185;
0; Mismatches 40; Indels 6
                                                                                                                                                                                                                                                                                                  1226 GCGCTGCCTGCCTTTCTGCTTTTGCCTGCTGCGAT 1266
                                                                                                                                                                                                                                                                                                                          736 GCGCTGCCTGCCTTTTTGCTGCATGGCTTTTTGCCTGCTGCTGT 776
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Best Local Similarity
Matches 802; Conserv
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ORGANISM: Zea mays
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; NAME/KEY: CDS
; LOCATION: (89).
US-10-042-894A-15
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                                                                                                                                                                                                                                                                                      Sequence 74436, Application US/10425115
| Publication No. US20040214272A1
| Sequence 74436, Application US/10425115
| Publication No. US20040214272A1
| GENERAL INFORMATION:
| APPLICANT: La Roas Thomas J.
| APPLICANT: Abou, Yinua APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Plants
| TITLE OF INVENTION: Plants | FILE REFERENCE: 38-21(53222) B | CURRENT APPLICATION NUMBER: US/10/425,115 | CURRENT FILING DATE: 2003-04-28 | NUMBER OF SEQ ID NOS: 369326 | LENGTH: 776
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CCTCCGAGTTGTGCTGGGTGTGGAGATCTGAGACGGTCGTCGGCCCCACTTGGTTGCCTTG 1045
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                                          841 GGCGGCTCTGCTCGCTGATCAAGTTCGTTTCTGACATTGTTCCGGAGACTCCTCATACG
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                                                                                                                                  901 CAGCCTTTGGGTCCTTCTTAAGAGGATCCTGGCA-TTTCGATTTGATAACAAAG 955
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  566 TCCGGCGCTACGTGTCATCCGTTGCCGACGAGGGGATGGACTGTGCGC
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US-10-425-115-74436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LOCATION: (1)..(776)
OTHER INFORMATION: unsure at all n locations
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA
ORGANISM: Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURE:
NAME/KEY: unsure
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US-10-042-894A-17
Sequence 17, Application US/10042894A
Sequence 17, Application VO. US2033009011A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Beach, Larry
APPLICANT: Rafalski, Antoni J.
APPLICANT: Cahoon, Rebecca E.
TITLE OF INVENTION: Genes and Uses Thereof
TITLE OF INVENTION: Genes and Uses Thereof
                                                                                                                                                                                                     187 CGGGGCCTTCTTCCCGCGCTTCCACGCACCCGCTTCCTCCCGGCCCCAGCCACCCC
                                                                                                                                                                                                                                                                                                            412 ATCGCCAAGTGCCTCGCCAAGGACCGCGGACCACGAGCGTTCTGCTCGGATTCCGCGTC
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              7 TCCGACCTGCCCCGCCCGAGCACCAGGTGGCGGGGCACCGCGCGCTCCGCCGAACTG
                                                 GGCCCGCTCATCGACGCCTCCTCCTACAAGCCGCTCCAGGCCGGCGACCGTGGG
                                                               67 GCCCCCTCCTCGTCGACGCGCGAGGGCTCTTCTACAAGCCCCTCCAGGCCGGGGAGCGCGGGG
                                                                                                   235 cgagacaccrrrcrrccccggrrccacgcacacacccccaccGagggGaggC-
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APPLICANT: La Rosa, Thomas J.
APPLICANT: Soulic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Wu, Wei
APPLICANT: Buckharov, Andrey A.
APPLICANT: Buckharov, Andrey A.
APPLICANT: Buckharov, Andrey A.
APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REPERENCE: 38-21(5321)B
CURRENT PILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NOS: 204966
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                                                               ATGGACTGTGCGCTCGCCGCGCGCGTTGTACGGAGGAAAAGGTGGAGTCTTGTCACAGCTG
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              ACATCAAGATCGGCGCCATCACGTGGCCACCGAGTTCGCCGGAGCCCTACATCGCCAAGT
                         399 ACATCAAGATCGGTGCCATCACGT------
                                                                                                                                                                      ACACCGCCGGCGTCCGCCGCGTGCTCCGGCGCTACGTGTCATCCG-TTGCCGACGAGGGG
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40.6%; Score 545.6; DB 19;
Best Local Similarity 78.6%; Pred. No. 4.7e-145;
Matches 695; Conservative 0; Mismatches 174;
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US-10-437-963-4650
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 4650, Application US/10437963 Publication No. US20040123343A1 GENERAL INFORMATION:
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Publication No. US20030009011A1
GENERAL INFORMATION:
APPLICANT: Shi, Jinrui
APPLICANT: Beach, Larry
APPLICANT: Rafalski, Antoni J.
APPLICANT: Rafalski, Antoni J.
APPLICANT: Cahoon, Rebecca E.
TITLE OF INVENTION: No. US2003009011A1e1 Inositol Polyphosphate Kinase
TITLE OF INVENTION: Genes and Uses Thereof
                                                                                                                                                                                                                                                                                                                                                                            169 GCCGTCCCGCCCCGGTGCCTCGCCAAGGACCGCGAAGCACCACCACGCGCGCTTC
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                                                                                                                                                                                                         Query Match 22.9%; Score 308; DB 19; Length 6
Best Local Similarity 69.6%; Pred. No. 2.4e-77;
Matches 451; Conservative 0; Mismatches 185; Indels
                                                                                                                                                          ; OTHER INFORMATION: Clone ID: PAT_MRT4530_11513C.1
US-10-437-963-4649
      FILE REFERENCE: 38-21(53221)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF ESQ ID NOS: 204966
SEQ ID NO 4649
LENGTH: 696
                                                                                                         TYPE: DNA
ORGANISM: Oryza sativa
FEATURE:
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US-10-042-894A-18
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APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Rou, Yahua
APPLICANT: Cao, Yongwei
APPLICANT: Wu, Wei
APPLICANT: Boukharov, Andrey A.
APPLICANT: Barbazuk, Brad
APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
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                                                                                                                                                                                                                                                                                          35.0%; Score 470.4; DB 14; Length 643; 95.9%; Pred. No. 1.1e-123;
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FILE REFERENCE: 1286
CURRENT APPLICATION NUMBER: US/10/042,894A
CURRENT FILING DATE: 2002-01-09
PRIOR PELING DATE: 2001-01-12
PRIOR FILING DATE: 2001-01-12
NUMBER OF SEQ ID NOS: 37
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 4649, Application US/10437963
Publication No. US20040123343A1
GENERAL INFORMATION:
                                                                                                                                                                                                                       LOCATION: (1)...(643)
OTHER INFORMATION: n = A, T, C or
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Best Local Similarity 95.9
Matches 509; Conservative
                                                                                                                                                                                                     NAME/KEY: misc feature
                                                                                                                                                      TYPE: DNA
ORGANISM: Zea mays
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                                                                                                                                        LENGTH: 643
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US-1U-U42-894A-19
; Sequence 19, Application US/10042894A
; Publication No. US20030009011A1
; GENERAL INFORMATION:
; APPLICANT: Shi, Jinrui
APPLICANT: Wang, Hongyu
; APPLICANT: Wang, Hongyu
; APPLICANT: Cahoon, Rebecca E.
; TITLE OF INVENTION: No. US2003009011A1e1 Inositol Polyphosphate Kinase
; TITLE OF INVENTION: Genes and Uses Thereof
; TITLE OF INVENTION: Genes and Uses Thereof
; FILE REFERENCE: 1286
; CURRENT APPLICATION NUMBER: US/10/042,894A
; CURRENT PILING DATE: 2002-01-09
; PRIOR APPLICATION NUMBER: US 60/261,465
; PRIOR PILING DATE: 2001-01-12
; NUMBER OF SEQ ID NOS: 37
; SQCTURARE FREESE for Windows Version 4.0
; SEQ ID NO 19
; LENGTH: 353
; TYPE: DAA
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14.3%; Score 191.6; DB 14; Length 353;
Best Local Similarity 90.2%; Pred. No. 3.1e-44;
Matches 238; Conservative 0; Mismatches 21; Indels 5;
                                                                                                                                                Query Match 16.4%; Score 220.8; DB 20; Length 295; Best Local Similarity 82.3%; Pred. No. 1.4e-52; Matches 237; Conservative 0; Mismatches 51; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     248 dehásásahadacchnásachccáccásásanccáccácacaccccasaca 295
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    ; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_109799C.1
US-10-425-115-10743
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LOCATION: (1)...(353)
OTHER INFORMATION: n = A, T, C, or G
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| Publication No. US20040214272A1
| GENERAL INFORMATION:
| GENERAL INFORMATION:
| APPLICANT: La Rosa, Thomas J.
| APPLICANT: Cao, Yongwai;
| TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
| TITLE OF INVENTION: Plants
| TITLE OF INVENTION: Plants
| TITLE OF INVENTION: WIMBER: US/10/425,115
| CURRENT PILING DATE: 2003-04-28
| UMMER OF SEQ ID NOS: 369326
| SEQ ID NO 10743
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 687 GCAGACTCTGTTCCACTTCTACTCGGCGTCGATTCTTCTGGGCTATGATGCTGCTGCTGCAGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 298.4; DB 14; Length 519;
Pred. No. 1.2e-74;
0; Mismatches 38; Indels 1;
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LOCATION: (1)..(295)
OTHER INFORMATION: ungure at all n locations
FILE REPERENCE: 1286
CURRENT APPLICATION NUMBER: US/10/042,894A
CURRENT FILING DATE: 2002-01-09
PRIOR APPLICATION NUMBER: US 60/261,465
PRIOR FILING DATE: 2001-01-12
NUMBER OF SEQ ID NOS: 37
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 18
LENGTH: 519
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LOCATION: (1)...(519)
COTHER INFORMATION: n = A, T, C, or G
US-10-042-894A-18
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Best Local Similarity 89.4%;
Matches 328; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: misc feature
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ORGANISM: Zea mays
                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA
ORGANISM: Zea mays
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US-10-425-115-10743
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completed: June 17, 2005, 04:00:54
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Publication No. USZ0030009011A1

GENERAL INFORMATION:

APPLICANT: Bach, Larry

APPLICANT: Bach, Larry

APPLICANT: Mang, Hongyu

APPLICANT: Mang, Hongyu

APPLICANT: Mang, Hongyu

TITLE OF INVENTION: No. USZ003009011A1e1 Inositol Polyphosphate Kinase

TITLE OF INVENTION: Genes and Uses Thereof

FILE REFERENCE: 1286

CURRENT APPLICATION NUMBER: US/10/042,894A

CURRENT FILING DATE: 2002-01-09

PRIOR FILING DATE: 2001-01-12

NUMBER OF SEQ ID NOS: 37

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 11

LENGTH: 1195
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55.6%; Pred. No. 4.2e-42;
cive 0; Mismatches 349; Indels 27;
                                                                                                                                                      AGCCTTTGGGTCCTTCTTAAGAGA
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ORGANISM: Eucalyptus grandis
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Matches 471; Conservative
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; LOCATION: (116)...(1048)
US-10-042-894A-11
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                                                                                                                                                                        GTGGAGTCTTGTCACAGCTGCGCGAGCTCAAGGCGTGCTTCGAGGAGCAGACTCTGTTCC
                                      761 ATGGGGGTGGGGTGACGGTGAAGCTGGTGGACTTTGCCCCATGTGGCCGAGGGTGATGGGG
AGGCCATGGACACCGCCGGCGTCCGCCGTGCTCCGGCGCTACGTGTCATCC-
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CC344833 OGIAQ20TV
CG450397 OGYCI27TV
CG453578 OGYAD20TV
CC344824 OGIAB23TV
CC124960 OGIAB23TV
CC124480 SCUFRT106
CG284572 OGWIF61TH
CG776236 1123005E0
CA24555 SCORTI100
CA130685 SCCCRT100
AX109355 Zea mays
CA20412 SCRIPL100
CC724950 OGIAB23TH
BZ774817 1151a11.b
CC134959 PUJCG54TD
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0		RESULT 1 CC344833 LOCUS DEFINITION	ACCESSION VERSION KEYWORDS SOURCE	ORGANIS	SS I	COMMENT	FEATURES SOUTCE	ORIGIN	Query Match Best Local Matches 92	Qy Dp

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/organism="Zea mays"
/organism="Zea mays"
/mol type="genomic DNA"
/strain="B73"
/db_xref="taxon:4577"
/clone="ZMMBNa0798B05"
/clone="ZMMC0 7 1.5 KB"
/note="ZM-Octor: pBGSK-; Site 1: HincII; 0.7-1.5 kb
methylation filtered genomic DNA library"
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9712 Medical Center Drive, Rockville, MD
9713 01-838-5843
Fax: 301-838-0208
Email: whitelaw@tigr.org
Panicoideae; Andropogoneae; Zea
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Class: sheared ends
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OGYCI27TV ZM_0.7_1.5_KB Zea mays genomic clone ZMMBMa0788E05,
genomic survey sequence.
CG240397.1 GI:34140283
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
(back, Panicoideae; Andropogoneae; Zea.
Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T.,
Resnick, A., Fraser, C.M., Budiman, M.A., Bedell, J.A., Rohlfing, T.,
Citerk, R.W., Nunberg, A., Robbins, D. and Lakey, N.
Unpublished (2002)
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Fax: 301-838-0208
Fax: 301-838-0208
Email: whitelaw@tigr.org
Seq primer: TR
Class: sheared ends.
Location/Qualifiers
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TIGR
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnollophyta; Liliopsida; Poales; PaccaD
clade; Panicoideae; Andropogoneae; Zea.

Mitclaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T.,

Resnick, A., Fraser, C.M., Budiman, M.A., Bedell, J.A., Rohlfing, T.,
Citck, R.W., Numberg, A., Robbins, D. and Lakey, N.

Consortium for Maize Genomics

AL Unpublished (2002)
Other_GSSs: OG9AD40TH
Contact: Cathy Whitelaw
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//organism="Zea mays"
//organism="Zeanomic DNA"
//organism="B73"
//bb_xref="taxon:4577"
//clone="ZmMsha080480108"
//clone="Ib="ZM 0.7 1.5 KB"
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llarity 99.6%; Pred. No. 2e-168;
Conservative 0; Mismatches 3; Indels 0
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Class: sheared ends.
Location/Qualifiers
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Fax: 301-838-0208
Email: whitelaw@tigr.org
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Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACCAD
clade, Panicoideae, Andropogoneae, Zea.
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Mitchaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T.,
Resnick, A., Fraser, C.M., Budiman, M.A., Bedell, J.A., Rohlfing, T.,
Citek, R.W., Nunberg, A., Robbins, D. and Lakey, N.
Consortium for Maze Genomics
Unpublished (2002)
Other_GSSs: OGLAB23TH
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/clone_lib="ZM_0.7_1.5_KB"
/note="Vector: pBCSK-; Site_1: HincII; 0.7-1.5
methylation filtered genomic_DNA_library"
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al Similarity 89.4%; Score 644.8; DB 9;
al Similarity 89.4%; Pred. No. 8.4e-141;
753; Conservative 0; Mismatches 27;
                                                                                                                                                                                                                                                                                                                                                                                                                     /mol_type="genomic DNA" /strain="B73"
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/organism="Zea mays"
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Class: sheared ends.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                     Fax: 301-838-0208
Email: whitelaw@tigr.org
                                                                                                                                                                                                                                     Contact: Cathy Whitelaw
 GI:32143893
                                                                                                                                                                                                                                                                                      Tel: 301-838-5843
 CC724960.1
GSS.
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                                                  Zea mays
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Genomic survey sequence.
CC724960
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                                                                                                 /note="Vector: pBCSK-; Site 1: HincII; 0.7-1.5 methylation filtered genomic DNA library"
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                                                                                                                                                                   Length 873
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                                                                                                                                                                     Score 752; DB 8; Le
Pred. No. 5.1e-166;
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                                                                /clone="ZMMBMa0359C15"
/clone_lib="ZM_0.7_1.5_KB"
/note="Vector: pBCSK-; Sit
               /mol_type="genomic DNA"
/strain="B73"
                                                  /db xref="taxon:4577"
 'organism="Zea mays
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CG284572 T19 bp DNA linear GSS 25-AUG-2003 OGWIF61TH ZM_0.7_1.5_KB Zea mays genomic clone ZMMBMa0584K02, genomic survey sequence.
CG284572 GI:34198786
GSS.
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construction can be obtained at
http://sucest.lad.ic.unicamp.br/public"
                                                                                              Score 620; DB 6; L
Pred. No. 5.7e-135;
0; Mismatches 82;
                                                                                                      46.1%;
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Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACCAD
clade, Panicoideae, Andropogoneae, Saccharum, Saccharum officinarum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CA114480 801 bp mRNA linear EST 24-SEP-2003
SCJFRT1061H11.g RT1 Saccharum officinarum cDNA clone SCJFRT1061H11
5', mRNA sequence.
CA134480
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/note="Organ: Root tips (0.3cm-long) from adult plants;
/note="Organ: Root tips (0.3cm-long) from adult plants;
/ector: psport1; Site 1: Sali; Site 2: Not1; An
unidirectional Dibrary generated from (Root tips
(0.3cm-long) from adult plants]. cDNA was prepared from
polyA+ mRNA using SuperScript Plasmid System Kit
(Invitrogen). The double-strand cDNAs were fractionated
in a sepharose Ci-2B 40cm-columns and fragments sizing
between 0.8 and 1.5 Kb were directionally cloned into the
vector. Details of each source of RNA and library
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Clone distribution: clone distribution information can be found
through the Brazilian Clone Collection Center (BCCC) at
http://www.bcccenter.fcav.unesp.br
Plate: 061 row: H column: 11
Seq primer: T7 Promoter Primer.
                                                                                                                                                                                                                                                                                                                                                                                                                                        AAGCTGGTGGACTTTGCCCATGTGGCCGAGGTGATGGGGTGATTGACCACAACTTCCTG
                                                         CGCGAGCTCAAGGCGTGGTTCGAGGAGCAGACTCTGTTCCACTTCTACTCGGCGTCGATT
                                                                                                                                                                                                                                                               CGCGAGCTCAAGGCGTGGTTCGAGGGGCAGACTCTGTTCCACTTCTACTCGGCGTCGATT
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                                                                                                                                                                                                                                                                                                                                                                      CTTCTGGGCTATGATGCTGCAGCAGCAGCAGCGGAGGTGGGGGTGGGGTAACAGTG
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                                                                                                                                   ATGGACTGTGCGCTCCCCCCCCCCGCGTGTACGGAGAAAAGGTGGAGTCTTGTCACAGCTG
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Vettore, A.L., da Silva, F.R., Kemper, B.L. and Arruda, P. The libraries that made SUCEST
Genet. Mol. Biol. 24 (1-4), 1-7 (2001)
Contact: Arruda P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Centro de Biologia Molecular e Engenharia Genetica
Universidade Estadual de Campinas
Gaixa Postal 6010, 13083-970, Campinas SP, Brazil
Tel: 55 19 3788 1137
Fax: 55 19 3788 1089
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/mol_type="mRNA"
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/clone="SCJFRT1061H11"
/lab host="DH10B"
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CA134480
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634 615

435 514 495 574 555

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/ clone libe="lal23" RescueMu Grid L"
/clone libe="lal23" RescueMu Grid L"
/note="Organ: leaf; Vector: RescueMu (engineered from
/note="Organ: leaf; Vector: RescueMu (engineered from
pBlueScript backbone); Site 1: BamHI; Site 2: BgIII;
RescueMu is a 4.9 Kb, modified maize Mu transposon
designed to allow plasmid rescue from total genomic DNA.
Mu elements insert preferentially into transcription
units: For more information on RescueMu, go to the web
site 'www.zmdb.iastate.edu' and RescueMu, go to the web
site 'www.zmdb.iastate.edu' and Rollow the links for
'RescueMu.' Grid Lwas grown in Molokai in 2001. DNA was
extracted from leaf strips, double digested using BamHI
and BgIII, and ligated to form circular plasmids. DH10B
cells were transformed and then screened on LB plates with
ampicillin."
                                                                                                                                                                                                                                                                                                                                                                                                                GSS 29-OCT-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Maize genomic sequences found using engineered RescueMu transposon Unpublished (2001) Contact: Walbot V
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Bermatophyta, Pagermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACCAD clade, Panicoideae, Andropogoneae, Zea.
546 Trercacaerrecedaecreaagecereerreaagecarreagecaeacrererrerrerae
                                                                                                                                                                                     606 TCGGCGTCGATTCTTCTGGCCTATGATGCTGCTGCAGTCGCAGCAGCGGGGGGT
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/cultivar="mixed background W23/A188/B73/K55"
/tissue_type="leaf"
/tissue_type="leaf"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 591;
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Stanford University
Stanford University
Fas: Galifornia Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
Email: walbordestanford.edu
Plate: 1123005 column: 3
Class: transposon.tagged.
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llarity 99.8%; Pred. No. 8.7e-128;
Conservative 0; Mismatches 1;
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organism="Zea mays"
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/lab_host="DH108"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GI:38034108
                                                                                                                                                                                                                                                                                                                                                                                                                                                            survey sequence.
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CG776236.1
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nes 590; Conserv
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                                            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
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                                                                                                           Tosses 1 to 719)
Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T.,
Resnick, A., Frser, C.M., Budiman, M.A., Bedell, J.A., Rohlfing, T.,
Citck, R.W., Nunberg, A., Robbins, D. and Lakey, N.
Consortium for Maize Genomics
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/clone="b=zxw 0.7_1.5 KB"
/note="Vector: pBcSK.; Site 1: HincII; 0.7-1.5 kb
methylation filtered genomic DNA library"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 719;
                                                                                                                                                                                                                                                                                                              73712 Medical Center Drive, Rockville, MD 20850, USA Tel: 301-838-5843
Fax: 301-838-0208
Email: whitelaw@tigr.org
Seq primer: TR
Class: sheared ends.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /mol_type="genomic DNA"
/strain="B73"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1. .719
/organism="Zea mays"
                                                                                                                                                                                                                          Unpublished (2002)
Other GSSs: OGWIF61TV
Contact: Cathy Whitelaw
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Matches 700; Conservat
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us-10-042-894a-7.rst

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/dione lib="Saccharum officinarum FLS"
/dione lib="Saccharum officinarum FLS"
/note="Organ: Developed inflorescence (20cm-long) without rachis; vector: pSport1; Site 1: Sal1; Site 2: Not1; An unidirectional cDNA library generated from Tbeveloped inflorescence (20cm-long) without rachis]. cDNA was prepared from polyA+ mRNA using SuperScript Plasmid System Kit (Invircogen): The double-strand cDNAs were fractionated in a sepharose CL-2B 40cm-columns and fragments sizing between 0.8 and 1.5 Kb were directionally cloned into the vector. Details of each source of RNA and library construction can be obtained at http://sucest.lad.ic.unicamp.br/public"
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RT1 Saccharum officinarum cDNA clone SCCCRT1004G05
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llarity 93.7%; Pred. No. 6e-122;
Conservative 0; Mismatches 39;
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5', mRNA sequence.
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Spermatophyta; Magnoliophyta; Lillopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Saccharum; Saccharum officinarum
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Centro de Biologia Molecular e Engenharia Genetica
Universidade Estadual de Campinas
Caixa Postal 6010, 13083-970, Campinas SP, Brazil
Tel: 55 19 3788 1089
Email: parruda@ounicamp.br
Clone distribution: clone distribution information can be found through the Brazilian Clone Collection Center (BCCC) at
                                                                                                                                                                                                                                                          ACGCGACTCCTCCCCACCGAGGCGCAGCCCGGGGAGCCGCATCCTCACTCGTCCTCGAC
                                                                                      TACAAGCCGCTCCAGGCCGGCGACCGTGGGGGACACGAGGTCGCCTTCTATGAGGCGTTC
                                                                                                                                                                         TCGGCCCACGCCGCCGTCCCGGCCCGCATCCGAGACACCTTCTTCCCCCGGTTCCACGGC
                                                                                                                                                                                                                                  ACGCGACTCCTCCCCACCGAGGCGCAGCCCGGGGAGCCGCATCCTCACCTCGTCCTCGAC
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Vettore, A. L., da Silva, F. R., Kemper, B. L. and Arruda, P. The libraries that made SUCEST
Genet. Mol. Biol. 24 (1-4), 1-7 (2001)
Contact: Arruda P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CTCCGGCGCTACGTGTCATCCGTTGCCGACGAGGGATGGACTGTGCGCTC

    . 656
    /organism="Saccharum officinarum"

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Plate: 081 row: A column: 03
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/db_xref="taxon:4547"
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CA245555.1 GI:35324301
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Submitted (15-APR-2002) Maize Mapping Project, University of Missouri, Columbia, MO 65211, USA

If you are interested in getting corresponding physical clones, these are publicly available from ZmDB and may be found by BLAST searching at MSL, maizemap.org; ZmDB, www.zmdb.iastate.edu; TIGR, www.igr.org; or NCBI, www.ncbi.nlm.nih.gov. When the source of the maize cDNA sequences is either Virginia Walbot, Stanford or Pat www.zmdb.iastate.edu.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HTC 17-0CT-2002
375 TCGCCGGAGCCCTACGTCGCCAAGTGCCTCGCCAAGGACCGCGGGACCACGAGCATTCTG 434
                                                                                                                                                                                                517 GAGGGCCCGGAGGTGAAGGCCATGGACACCGCCGGCGTCCGCCGCGCGTGCTCCGGCGCTAC 576
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Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACCAD
clade, Panicoideae, Andropogoneae, Zea.
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                                                                   CTCGGATTCCGCGTCTCCGAGTCGTCGGCCCCCGAGGGCCCCGTGTGGCGGACG
                                                                                                                                                                                                                                     495 GAGCGCCCGGAGGTGAAGGCCCTGGACACCGCCGGCGTCCCCCCGCGTGCTCTTA
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Hainey, C.F., Dolan, M., Miao, G.H., Vogel, J.M., Whitsitt, M.S., Arthur, L.W., Hanafey, M., Morgante, M. and Tingey, S.V.
Maize Mapping Project/DuPont Consensus Sequences for Design of Overgo Probes
Overgo Probes
Unpublished (2002)
2 (bases 1 to 3374)
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67.7%; Pred. No. 2.8e-120;
ive 0; Mismatches 259;
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/db_xref="MalzeDB:632179"
/db_xref="taxon:4577"
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                                                                                                                                                                                                                                                                                                                                             Centron de Biologia Molecular e Engenharia Genetica
Universidade Estadual de Campinas
Caixa Postal 6010, 13083-970, Campinas SP, Brazil
Tel: 55 19 3788 1137
Fax: 55 19 3788 1139
Fax: 55 19 3788 1089
Email: parruda@unicamp.br
Clone distribution: clone distribution information can be found through the Brazilian Clone Collection Center (BCCC) at http://www.bcccenter.fcav.unesp.br
Plate: 004 row: G column: 05
Seq primer: T7 Promoter Primer.
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                                                                                                                                                                                                                              Vettore, A.L., da Silva, F.R., Kemper, E.L. and Arruda, P.
The libraries that made SUCEST
Genet. Mol. Biol. 24 (1-4), 1-7 (2001)
Contact: Arruda P
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CA202412 671 bp mRNA linear EST 25-SEP-2003 SCRLFL1009H02.g FL1 Saccharum officinarum cDNA clone SCRLFL1009H02

RESULT 12 CA202412 LOCUS DEFINITION

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/nccom_line_line_line
(lcm-long); vector: pSport1; Site_1: Sal1; Site_2: Not1;
An unidirectional cDNA library generated from
Linelorescence at begining of development (lcm-long)].
CDNA was prepared from polyA+ mRNA using SuperScript
Plasmid System Kit (invitrogen). The double-strand cDNAs
were fractionated in a sepharose CL-2B 40cm-columns and
fragments sizing between 0.8 and 1.5 Kb were
directionally cloned into the vector. Details of each
source of RNA and library construction can be obtained at
http://sucest.lad.ic.unicamp.br/public"
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Vettore, A.L., da Silva, F.R., Kemper, B.L. and Arruda, P.
The libraries that made SUCEST
Genet. Mol. Biol. 24 (1-4), 1-7 (2001)
Contact: Arruda P
Contro de Biologia Molecular e Engenharia Genetica
Universidade Estadual de Campinas
Caixa Poetal 6010, 13083-970, Campinas SP, Brazil
Tel: 55 19 3788 1037
Fax: 55 19 3788 1037
Fax: 55 19 3788 1030
Fax
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Bukaryota, Viidiblantee, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
Slade; Panicoideae; Andropogoneae; Saccharum; Saccharum officinarum
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/clone="SCRLFL1009H02"
/lab_host="DH108"
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90.2%; Pred. No. 1.1e-119;
ive 0; Mismatches 65;
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                                       CA202412
CA202412.1 GI:35237651
EST.
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                                                                                 CAAGATCGGCGCCATCACGTGGCCACCGAGTTCGCCGGAGCCCTACATCGCCAAGTGCCT 425
                                                                                                                                                                                                                TCCTCACCTCGTCGTCGACGACCTCGCGGGGTTTCAGGCGCCCTGCGTCGCAGACAT
                                          CGTCGGCCCCCGAGGCGCCGTGTGGCGGACGGAGCCCCCGGAGGTGAAGGCCATGGACAC
                                                                                                                                       426 CGCCAAGGACCGCGGACCACGAGGGTTTCTGCATTCCGCGTCTCCGAGT
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OGLAB23TH ZM_0.7_1.5_KB Zea mays genomic clone ZMMBMa0307C22,
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1 (bases 1 to 722)
Mithelaw,C.A., Quackenbush,J., Van Aken,S., Utterback,T., Resnick,A., Fraser,C.M., Budiman,M.A., Bedell,J.A., Rohlfing,T., Citek,R.W., Nunberg,A., Robbins,D. and Lakey,N.

Consortium for Maize Genomics
Unpublished (2002)
Other GSSs: OGLAB23TV
                           591
                                          651
                                                                                                 TCACAGCTGCGCGAGCTCAAGGCGTGCTTCGAGGAGCAGACTCTGTTCCACTTCTACTCG 711
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                                                                                                                                                                                              GCGTCGATTCTTCTGGGCTATGATGCTGCTGCAGTCGCAGCAGCGGGAGATGGGGGGTGGG 771
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                                                                                                                                                                                                                                                                                602 TIGAAGGIGAA-CIIGITGACTITITCCCATITIGICAAGITGAIAGGGGGAAIGAACCA 660
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TCCGGCGTCCGGGTCGTCCCGAGGGCGCCGTGTGGCGGACTGAGCGCCCCGGAGGTG 361
                                                                                 GACGAGGGGATGGACTGTGCGCTCGCCGCGCGGTGTACGGAGGAAAAGGTGGAGTCTTG
                                                                                                                                                                                                                          542 GCGGTGAATCTTTTGGGCTATGATGCTAGTGCAAGTGCAGCAAGCGGAGGTGAAGGTGG
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methylation filtered genomic DNA library"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-5843
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
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CC724950
CC724950.1 GI:32143883
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Email: whitelaw@tigr.org
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Class: sheared ends.
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661 AAATTTCTGGG 671
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B2774817 593 bp DNA linear GSS 14-MAR-2003 ii51a11.bl WGS-ZmaysF (DH5a methyl filtered) Zea mays genomic clone li51a11, genomic survey sequence. B2774817 GI:28952260 478 358 238 118 604 418 664 784 844 178 724 357 AGCTCAAGGCGTGGTTCGAGGGCCAGACTCTGTTCCACTTCTACTCGGCGTCGATTCTTC 298 904 Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACCAD clade, Panicoideae, Andropogoneae, Zea. 477 TGTCGGCGTCCGCCGCGTGCTCCGGCGTACGCTTGCCGACGACGAGGGATGG 297 resecrargargerecrecaerecaecaecaecaegaegreegegraagereaegraacaereaage TGGTGGACTTTGCCCATGTGGCCGAGGTGATGGGGTGATTGACCACAACTTCCTGGGCG TGGTGGACTTTGCCCATGTGGCCGAGGGTGATGGGGTGATTGACCACAAACTTCCTGGGCG GGCTCTGCTCGCTGATCAAGTTCGTTTCTGACATTGTTCCGGAGACTCCTCATACGCAGC 546 CGCCGGCGTCCGCCGCGTCCGGCGCTACGTGTCATCCG-TTGCCGACGAGGGGATGG AGCTCAAGGCGTGGTTCGAGGAGCAGACTCTGTTCCACTTCTACTCGGCGTCGATTCTTC TGGGCTATGATGCTGCTGCAGTCGCAGCCAGAGATGGGGGTGGGGTGACGGTGAAGC Actignececrocecececegeneracecaaecaaecaecacerorrercacaececece Dedhia, N., Nascimento, L., E 1 (bases 1 to 593)

S Rabinowicz, P.D., O'Shaughnessy, A.L., Balija, V., Dedhia, N., Karzenburger, F., King, L., Miller, B., Muller, S., Nascimento, L. Zutzerburger, F., King, L., Miller, B., Muller, S., Nascimento, L. Zutavern, T., McCombie, W.R. and Martiensen, R.A. Genomic shotgun sequences from Zea mays (methyl-filtered) Unpublished (2002)

Contact: W. Richard McCombie

Lita Annenberg Hazen Genome Sequencing Center
Cold Spring Hazen Genome Sequencing Center
Cold Spring Hazen Genome Sequencing Tel: 516 367 8884

Fax: 516 367 8884

Fax: 516 367 8884

Email: mccombie@cshl.org CTTTGGGTCCTTCTTAAGAGAGGATCCTGGCA-TTTCGATTTGATAACAAAG 955

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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Saccharum; Saccharum officinarum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="Organ: Root tips (0.3cm-long) from adult plants;
Vector: pSport1; Site 1: Sal1; Site 2: Not1; An
unidirectional cDNA library generated from [Root tips
(0.3cm-long) from adult plants]. cDNA was prepared from
poly4-mRNA using SuperScript Plasmid System Kit
(Invitrogen). The double-strand cDNAs were fractionated
in a sepharose CL-2B 40cm-columns and fragments sizing
between 0.8 and 1.5 Kb were directionally cloned into the
vector. Details of each source of RNA and library
construction can be obtained at
                                                                                                                                                                                                                                                                                                                                                        Email: parruda@unicamp.br
Clone distribution: clone distribution information can be found
through the Brazilian Clone Collection Center (BCCC) at
http://www.bcccenter.fcav.uneap.br
Plate: 004 row: G column: 06
Seg primer: T7 Promoter Primer.
Location/Qualifiers
                                                                                                                                                                   1 (bases 1 to 744)
Vettore, A. L., da Silva, F.R., Kemper, E.L. and Arruda, P. The libraries that made SUCEST
Content. Mol. Biol. 24 (1-4), 1-7 (2001)
Contact: Arruda P
                                                                                                                                                                                                                                              Contact: Arruda P
Contro de Biologia Molecular e Engenharia Genetica
Centro de Biologia Molecular e Engenharia Genetica
Universidade Estadual de Campinas SP, Brazil
Caixa Postal 6010, 13083-970, Campinas SP, Brazil
Tel: 55 19 3788 1039
Fax: 55 19 3788 1089
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1. .744
// Organisma="Saccharum officinarum"
// mol_type="mRNA"
/db_xref="taxon:4547"
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/lab host="DH10B"
/clone lib="RT1"
                   GI:35013916
                                                       Saccharum officinarum
                                                                            Saccharum officinarum
 CA130686
CA130686.1
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VERSION
KEYWORDS
SOURCE
ORGANISM
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AUTHORS
TITLE
JOURNAL
COMMENT
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                                                                                                                                                                                                                              /clone_ib="WGS-ZmaysF (DHSa methyl filtered)"
/note="Organ: immature ears; Site_1: Xba I; Site_2: Xba I;
The vector was digested with Xba! and one nucleofide was
added by fill in the recessive 3' end. The genomic DNA
was nebulized, end repaired, adaptor ligated and size
fractionated using sephadex. The resulting fragments were
between 0.8 and 3 kb and were cloned into the vector (:x/y
reads in Mi3mpl9. .b/g reads in pUC19). The same ligation
was transformed into DHSa."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CGGCGACCGTGGGGAGCACGAGGTCGCCTTCTATGAGGCGTTCTCCGCCCACGCCGCTT
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/organism="Zea mays"
/mol_type="genomic DNA"
/cultivar="B73"
Plate: ii51 row: a column: 11
Seq primer: -21M13UnivFwd
Class: shotgun
High quality sequence stop: 593.
Location/Qualifiers
                                                                                                                                                                         /db_xref="taxon:4577"
                                                                                                                                                                                             /clone="ii51all"
/lab_host="DH5a"
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Matches 564; Conservative
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                                                                                                                                16 CETCTCGCCCTCACCATGTCCGACCT-CGCCCGCGGAGCACCACGAGGCGCCGGCCGCCGC
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                                                                                                              37 CCCCTTCCCCATACCATGTCCGACCTCCACCCGGGGGGGCCCAAGTCGCCGGCCACCGC
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                                                                                                                                                                                                                                                                           CCCACCGAGGCGCAGCCGGGGAGCCGCATCCTCACCTCGTCCTCGACGACCTCCTCGCG
                                                                                 Gaps
                                                                               .:
                                                 Length 744;
                                             Score 525.6; DB 6; Length
Pred. No. 9e-113;
0; Mismatches 74; Indels
http://sucest.lad.ic.unicamp.br/public"
                                                 39.1%;
                                                 Query Match 39.1
Best Local Similarity 88.6
Matches 592; Conservative
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CA130686 SCCRT1004G06.g RT1 Saccharum officinarum cDNA clone SCCCRT1004G06 5', mRNA sequence.

RESULT 15 CA130686 LOCUS DEFINITION

Search completed: June 17, 2005, 01:52:45 Job time : 4778 secs us-10-042-894a-7.rni

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Sequence 687, App
Sequence 881, App
Sequence 1, Appli
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Sequence 5, Appli
Sequence 1318, Ap
Sequence 1154, Ap
Sequence 1147, Ap
Sequence 1147, Ap
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1, Appli
3, Appli
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Sequence 13679, A
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Sequence 19, Appl
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                                                                                                                                    (without alignments)
8658.094 Million cell updates/sec
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                                                                                                                                                                                     Sequence 4, A
Sequence 2, A
Sequence 5, A
Sequence 2,
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Sequence 3,
Sequence 2
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                                                                                                                    June 16, 2005, 22:35:02 ; Search time 254 Seconds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
/cgn2_6/ptodata/1/ina/5B_COMB.seq:*
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                 GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-09-949-016-13686
US-09-949-016-13679
US-09-902-540-687
US-09-902-540-687
US-09-902-540-687
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US-09-902-540-1154
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US-09-902-540-1147
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US-08-528-199-2
US-08-528-199-5
US-09-103-840A-2
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Maximum Match 100%
Listing first 45 summaries
                                                                                nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 200000000
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Match Length DB
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Sequence 177, App
Sequence 182, Appli
Sequence 7871, Ap
Sequence 788, Appli
Sequence 9, Appli
Sequence 6598, Ap
Sequence 6598, Ap
Sequence 6519, Ap
Sequence 6519, Ap
Sequence 1190, Ap
Sequence 77, Appli
Sequence 7, Appli
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Sequence 4, Application US/09249585A
SERENTAL INFORMATION:
APPLICANT: HORLICK, Robert
TITLE OF INVENTION: METHOD FOR MAINTENANCE AND SELECTION OF EPISOMES
FILE REFERENCE: 0867/0D905
CURRENT APPLICATION NUMBER: US/09/249,585A
CURRENT FILING DATE: 1999-02-11
NUMBER OF SEQ ID NOS: 18
SOFTWARS: PatentIn version 3.0
SEQ ID NO 4
LENGTH: 1926
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Pred. No. 7.8e-07;
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US-09-056-556-182

US-09-072-596-177

US-09-072-967-182

US-09-102-840-781

US-09-902-540-781

US-09-902-540-788

US-09-902-540-788

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US-09-902-540-1190
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; OTHER INFORMATION: template strand of EBNA-1 DNA US-09-249-585A-4
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Best Local Similarity 45.6%;
Matches 246; Conservative
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APPLICANT: Robbins, Alan K.
TITLE OF INVENTION: Bukaryotic Cells Stably Expressing Genes FITLE OF INVENTION: Prom Multiple Transfected Episomes FITLE REFERENCE: 0867/1D903US1
CURRENT APPLICATION NUMBER: US/09/130,114
CURRENT APPLICATION NUMBER: US/09/130,114
SOFTWENT FILING DATE: 1998-08-06
NUMBER OF SEQ ID NOS: 36
SOFTWARE: FastSEQ for Windows Version 3.0
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APPLICANT: BETLACH, Melanie C.
APPLICANT: BETLACH, Melanie C.
APPLICANT: BETLACH, Melanie C.
APPLICANT: BETLACH, Melanie C.
APPLICANT: BETLACH, Mary C.
APPLICANT: McDANIEL, Robert
TILLE OF INVERTION: RECOMBINANT NARBONOLIDE POLYKETIDE SYNTHASE
TITLE OF INVERTION: RECOMBINANT NARBONOLIDE POLYKETIDE SYNTHASE
TITLE OF INVERTION NUMBER: US/09/320,878
CURRENT APPLICATION NUMBER: US/09/320,878
CURRENT PILING DATE: 1999-05-27
EARLIER PILING DATE: 1998-06-26
EARLIER PILING DATE: 1997-04-30
EARLIER PILING DATE: 1997-04-30
EARLIER PILING DATE: 1997-02-08
EARLIER PILING DATE: 1998-05-26
EARLIER PILING DATE: 1998-05-28
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Sequence 19, Application US/09320878A Patent No. 6117659
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RESULT 6
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4.4%; Score 58.6; DB 4; Length 38506;
Best Local Similarity 44.9%; Pred. No. 0.00087;
Matches 223; Conservative 0; Mismatches 274; Indels 0;
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APPLICANT: BETLACH, Melanie C.
APPLICANT: BETLACH, Mary C.
APPLICANT: BETLACH, Mary C.
APPLICANT: BETLACH, Mary C.
APPLICANT: TANG, Li
TITLE OF INVENTION: RECOMBINANT NARBONOLIDE POLYKETIDE SYNTHASE
ITILE OF INVENTION: RECOMBINANT NARBONOLIDE POLYKETIDE SYNTHASE
FILE REFERENCE: 30062200120
CURRENT APPLICATION NUMBER: US/09/657,440
CURRENT APPLICATION NUMBER: 09/320,878
PRIOR PAPLICATION NUMBER: 09/320,878
PRIOR PLILNG DATE: 1999-08-28
PRIOR PILLNG DATE: 1999-08-28
NUMBER OF SEQ ID NOS: 34
SOFTWARE: PATENTIN VOR: 2.0
SEQ ID NO 19
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44.9%; Pred. No. 0.00087;
tive 0; Mismatches 274;
Sequence 19, Application US/09657440; Patent No. 6509455; GENERAL INFORMATION:
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Matches 223; Conservative
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Sequence 13679, Application US/09949016

Patent No. 6812339

GENERAL INFORMATION

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REFERENCE: CLOO1307

CURRENT FILING DATE: 2000-04-14

PRIOR PELLING DATE: 2000-10-20

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR PELLING DATE: 2000-10-03

PRIOR FILING DATE: 2000-0-06

PRIOR FILING DATE: 2000-10-03

SET OF SEC ID NOS: 207012

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 13679
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4.3%; Score 58.4; DB 4; Length 18235;
46.2%; Pred. No. 0.00076;
tive 0; Mismatches 226; Indels 0;
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 13686
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Matches 194; Conservative
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Best Local Similarity
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US-09-949-016-13679/c
                                                                                                                                                                                                                                                                                                                                                                                                    ; TYPE: DNA
; ORGANISM: Human
US-09-949-016-13686
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; ORGANISM: Human
US-09-949-016-13679
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US-09-49-016-13686/c
5 Sequence 13686, Application US/09949016
5 Sequence 13686, Application US/09949016
5 Patent No. 6812339
6 GENERAL INFORMATION:
7 TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
7 TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
7 FILE REFERENCE CL001307
7 CURRENT APPLICATION NUMBER: US/09/949,016
7 CURRENT FILING DATE: 2000-04-14
7 PRIOR APPLICATION NUMBER: 60/241,755
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                                                                                                                                                                    APPLICANT: FRASER, Claire M.
APPLICANT: VENTER, John C.
TITLE OF INVENTION: DAM SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM TITLE OF INVENTION: TUBERCULOSIS
FILE REFERENCE: 24366-20007.00
CURRENT APPLICATION NUMBER: US/09/103,840A
CURRENT FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PATENTIN VET. 2.1
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4.4%; Score 58.6; DB 3; Length 4411529;
Best Local Similarity 44.4%; Pred. No. 0.0042;
Matches 235; Conservative 0; Mismatches 294; Indels 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA
ORGANISM: Mycobacterium tuberculosis
OTHER INFORMATION: H37Rv
Patent No. 6294328
GENERAL INFORMATION:
APPLICANT: FLEISCHMAN, Robert D.
                                                                                                                                         WHITE, Owen R
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LENGTH: 4411529
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GCTCCGGCCTCTTCTACAAGCCGCTCCAGGCCGGCGACCGTGGGGAGCACGAGGTCGCCT 190
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FILE REFERENCE: 38-10(1549)B
CURRENT APPLICATION NUMBER: US/09/902,540
PRIOR APPLICATION NUMBER: 60/217,883
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; Sequence 4, Application US/09881165
; Patent No. 6632930
; GENERAL INFORMATION:
; APPLICANT: HOWARD, JOHN
; APPLICANT: HOWARD, JOHN
; APPLICANT: WANG, HUAMING
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; TITLE OF INVENTION: ENZYMES PRODUCED IN PLANTS
; TITLE OF INVENTION: ENZYMES PRODUCED IN PLANTS
; TITLE OF INVENTION: ENZYMES PRODUCED
; FILE REFERENCE: 1003-06-14
; FILE REPERENCE: 2001-06-14
; PRIOR PLIING DATE: 2000-06-15
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PATENTIN VUNIER: 2010-06-15
; SEQ ID NO 4
; LENGTH: 1082
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                                                                                                                                                                                                                                                                                                                                         Sequence 687, Application US/09902540

Patent No. 6833447

GENERAL INFORMATION:
APPLICANT: Goldman, Barry S.
APPLICANT: Slater, Steven C.
APPLICANT: Slater, Steven C.
TITLE OF INVENTION: Mycococcus xanthus Genome Sequences and Uses Thereof;
FILE REFERENCE: 38-10(15849)B

CURRENT APPLICATION NUMBER: US/09/902,540

CURRENT APPLICATION NUMBER: 02/01-07-10

PRIOR FILING DATE: 2001-07-10

PRIOR FILING DATE: 2000-07-10

WUMBER OF SEQ ID NOS: 16825
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1314 CCGGGTGGTGAAGGCGGACCAGCTGTCGGACCGCGGCTTCTTCTACCGGTCGGACCAGTT 1373
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Pred. No. 0.00061;
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                                                                              582 ATCCGTTGCCGACGAGGGGATGGACTGTGCGCTCGCCG
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Patent No. 6783969
GENERAL INFORMATION:
APPLICANT: Tang, Y. Tom
APPLICANT: Tang, V. Tom
APPLICANT: Goodrich, Ryle
APPLICANT: Asmudi, Vinod
APPLICANT: Ren, Feiyan
APPLICANT: Zhang, Jie
APPLICANT: Zhang, Jie
APPLICANT: Zhang, Jie
APPLICANT: Zhang, Jie
APPLICANT: Zhao, Qing A.
APPLICANT: Zhao, Qing A.
APPLICANT: Mang, Yunqing
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Best Local Similarity 48.23
Matches 163; Conservative
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US-09-902-540-687/c
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46.7%; Pred. No. 0.00074;
ive 0; Mismatches 209; Indels 0
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Patent No. 6340774

GRUBRAL INPORMATION:
APPLICANT: Stanford University
APPLICANT: Khosla, Chaitan

TITLE OF INVENTION: NON-STEROIDAL ESTROGEN-RECEPTOR
TITLE OF INVENTION: NON-STEROIDSTS
FILE REFERENCE: 28600-20210.00

CURRENT APPLICATION NUMBER: US 60/243,458

PRIOR APPLICATION NUMBER: US 60/243,458

PRIOR FILING DATE: 2000-01-25

PRIOR FILING DATE: 2000-01-25

PRIOR FILING DATE: 2000-01-31
                                                                                           APPLICANT: Wang, Dunrui
APPLICANT: Yang, Yonghong
APPLICANT: Wehrman, Tom
APPLICANT: Ghosh, Reena
APPLICANT: Drmanac, Radoje T.
TITLE OF INVENTION: No. 6783966el Nucleic Acids and
FILER REFERENCE: 803
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CURRENT FILING DATE: 2001-03-05
NUMBER OF EEQ ID NOS: 948
SOFTWARE: DL.FL.genes Version 2.0
SEQ ID NO 881
Yamazaki, Victoria
Chen, Rui-hong
Wang, Zhiwei
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Matches 183; Conservative
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; LOCATION: (330)..(4265)
US-09-799-451-881
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ORGANISM: Homo sapiens
FEATURE:
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ORGANISM: Streptomyces venezuelae
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LENGTH: 36778
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                                                                                                                                                                                                                                                                                                                                                                                                      Score 57.6; DB 3; Length 2. Pred. No. 0.0013; 0; Mismatches 184; Indels
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Patent No. 6265202

GENERAL INFORMATION:
APPLICANT: Sherman, D.H.
APPLICANT: Liu, H. H.
APPLICANT: Liu, Y.
APPLICANT: Liu, Y.
APPLICANT: Liu, Y.
APPLICANT: Liu, W.
TITLE OF INVENTION: DNA encoding methymycin and pik
TITLE PREERROKE: 600.438US1
CURRENT APPLICATION NUMBER: US/09/105,537A
CURRENT FILING DATE: 1998-06-26

CURRENT FILING DATE: 1998-06-26

CURRENT FILING DATE: 1998-06-26

SOFTWARE: PREES FOR SEQ ID NOS: 43

SEQ ID NO 32.
NUMBER OF SEQ ID NOS: 1
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1
                                                                                                                                                                                                                                                  ; OTHER INFORMATION: n = A,T,C or G
US-09-773-816-1
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Best Local Similarity 49.2%;
Matches 181; Conservative
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Matches 222; Conservative
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                                                                                                                                     TYPE: DNA
ORGANISM: Human
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; Sequence 5, Application US/09105537A
; Patent No. 6265202
; GENERAL INFORMATION:
; APPLICANT: Sherman, D.H.
; APPLICANT: Xue, Y.
; APPLICANT: Zhao, L.
; TITLE OF INVENTION: DNA encoding methymycin and pikromycin
; FILE REFERENCE: 600.4338US1
; CURRENT APPLICATION: US/09/105,537A
; CURRENT FILING DATE: 1998-06-26
; NUMBER OF SEQ ID NOS: 43
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Best Local Similarity 44.7%; Pred. No. 0.0021;
Matches 222; Conservative 0; Mismatches 275; Indels
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Search completed: June 17, 2005, 01:57:11 Job time : 267 secs

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/product= "Maize IPPK protein #4"
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polypeptides and polynucleotides. Sequences of the invention are useful in modulating the phytic acid biosynthesis by decreasing phytate and/or increasing non-phytate phosphorous to improve the nutritional value of animal feed, or to reduce the environmental impact of animal waste. Polynucleotides of the invention are to produce transgenic plants with altered phenotype. IPPK proteins are used to screen compounds that modulate their activity and raising anti-idiotypic antibodies. The
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Pred. No. 2.3e-271;
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                                                                                                          CAAGITITIGICIGGAAAAAGAAGCGCCTCCGAGITGIGCTGGGGTGIGGAGAICTGAGACG
                                                                                                                                                                             New inositol polyphosphate kinase polynucleotides and polypeptides, useful in modulating phytic acid biosynthesis by decreasing phytate increasing non-phytate phosphorous to improve the nutritional value
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                                               The invention relates to novel inositol polyphosphate kinase (IPPK) polypeptides and polymucleotides. Sequences of the invention are useful in modulating the phytic acid biosynthesis by decreasing phytate and/ or increasing non-phytate phosphorous to improve the nutritional value of animal feed, or to reduce the environmental impact of animal waste. Bolymucleotides of the invention are to produce transgenic plants with an altered phenotype. IPPK proteins are used to screen compounds that modulate their activity and raising anti-idiotypic antibodies. The
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Pred. No. 4.2e-171;
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                          Claim 1; Page 62-63; 86pp; English
                                                                                                                                                               present sequence is maize IPPK DNA
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llarity 98.8%;
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The invention relates to novel inositol polyphosphate kinase (IPPK) polypeptides and polymucleotides. Sequences of the invention are useful in modulating the phytic acid biosynthesis by decreasing phytate and/ or increasing non-phytate phosphorous to improve the nutritional value of animal feed, or to reduce the environmental impact of animal waste. Onlynucleorides of the invention are to produce transgenic plants with an altered phenotype. IPPK proteins are used to screen compounds that modulate their activity and raising anti-idiotypic antibodies. The
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nutritional value; animal feed; transgenic; gene; ds
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                                                                                                              TCCAGAGACTCCTCAGACGCAGCCTTTGGGTCCTTCTTAA
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Pred. No. 5.5e-167;
0; Mismatches 22;
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84. .806
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Matches 890; Conservative
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"Maize IPPK
Location/Qualifiers
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            CGGCGACCGTGGGGAGCACGAGGTCGCCTTCTATGAGGCGTTCTCCGCCCACGCCGCCGT
                         CGGCGACCGTGGGGGACACGAGGTCGCCTTCTATGAGGCGTTCTCCGCCCACGCGT
                                                        CCCGGCCCGCATCCGAGACACCTTCTTCCCCCGGTTCCACGGCACGCGACTCCTCCCCCAC
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nutritional value; animal feed; transgenic; gene; ds
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The invention relates to novel inositol polyphosphate kinase (IPPK) polypeptides and polynucleotides. Sequences of the invention are useful in modulating the phytic acid blosynthesis by decreasing phytate and/ or increasing non-phytate phosphorous to improve the nutritional value of animal feed, or to reduce the environmental impact of animal waste. Polynucleotides of the invention are to produce transgenic plants with saltered phenotype. IPPK proteins are used to screen compounds that modulate their activity and raising anti-idiotypic antibodies. The present sequence is maize IPPK DNA or of ATTCGCGTCTCCGGCGTCCGAGTCGTCGCCCGAGGGCGCCGTGTGGCGGAGCG CGCCAGCAAGCCGGGCCCGCTCATCGACGGCTCCGGCCTCTTCTACAAGCCGGTCCAGGC TCCCCATACCATGTCCGACCTCCACCCGGGGGCACCAAGTCGCCGGCCACCGCGCCTC CGCCAGCAAGCTGGGCCCGCTCATCGACGGCTCCGGCCTCTTCTACAAGCCGCTCCAGGC CGGCGACCGTGGGGACCACGAGGTCGCCTTCTATGAGGCGTTCTCCGCCCACGCCGCT CCCGGCCCGCATCCGAGACACCTTCTTCCCCCGGTTCCACGGCACGCGACTCCTCCCCAC CCGGGCCGCATCCGAGACACCTTCTTCCCCCGGTTCCACGGCACGCGGACTCCTCCCCAC CGAGGCGCAGCCCGCATCCTCACCTCGTCCTCGACGACCTCCTCGCGGGGTT TCAGGCGCCCTGCGCAGCCATCAAGATCGGCGCCCATCACGTGGCCACCGAGTTCGCC Gaps New inositol polyphosphate kinase polynucleotides and polypeptides, useful in modulating phytic acid biosynthesis by decreasing phytate increasing non-phytate phosphorous to improve the nutritional value animal feed. 1; 923; Sequence 923 BP; 138 A; 326 C; 286 G; 173 T; 0 U; 0 Other; Length Indels RE; 62.3%; Score 837.4; DB 6; llarity 97.5%; Pred. No. 1.9e-165; Conservative 0; Mismatches 21; #2# Cahoon protein Rafalski JA, 403 462 셤 ò

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                         CCCGGAGGTGAAGGCTATGGACACCGTCGGCGCCCCGCGCGTGCTCCGGCGCTACGTGTC
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141 an 121 181 201 241 261 301 321 361 381 421 405 481 446 541 506 900 566 99 626 720 989 780 746 840 806 841 GGCGGGCTCTGCTCGATCAAGTTCGTTTCTGACATTGTTCCGGAGACTCCTCATACG 900 61 81 ö The invention relates to novel inositol polyphosphate kinase (IPPK) polypeptides and polymucleotides. Sequences of the invention are useful in modulating the phytic acid biosynthesis by decreasing phytate and/or increasing non-phytate phosphorous to improve the nutritional value of animal feed, or to reduce the environmental impact of animal waste. Polymucleotides of the invention are to produce transgenic plants with a altered phenotype. IPPK proteins are used to screen compounds that modulate thair activity and raising anti-idiotypic antibodies. The present sequence is maize IPPK DNA rccaccecceascaccasarceccesrcacececcicceccaecascasecres CTTCTGGGCTATGATGCTGCTGCAGTCGCAGGCGGAGATGGGGGTGGGGTGACGGTG caccarceccaccecercaccecrrecreearag-----receearaccarecearec TCCACCCGCGGAGCACCAAGTCGCCGGCCACCGCGCCTCCGCCAGCAAGCTGGGCCCGC TCATCGACGGCTCCTCTTCTACAAGCCGCTCCAGGCCGGCGACCGTGGGGAGCACG rcarcaacacreredecrerretacaadececrecadecedeceacearedadeacace AGGICGCCTICTATGAGGCGTICTCCGCCCACGCCGCCGTCCCGGCCCGCATCCGAGACA AGGTCGCCTTCTATGAGGCGTTCTCCGCCCACGCCGCCGTCCCGGCCCGCATCCGAGACA CCTTCTTCCCCCGGTTCCACGGCACGCGACTCCTCCCCACCGAGGCGCAGCCCGGGGAGC CGCATCCTCACCTCGTCCTCGACGACCTCCTCGCGGGGTTTCAGGCGCCCTGCGTCGCAG ACATCAAGATCGGCGCCATCACGTGGCCACCGAGTTCGCCGGAGCCCTACATCGCCAAGT ACATCAAGATCGGTGCCATCACGT-----GAGTCGTCGGCCCCGAGGGCGCCGTGTGGCGGACGCGCCCCGGAGGTGAAGGCCATGG GAGTCGTCGGCCCCGAGGGCGCCGTGTGGCGGACGGAGCCCCCGGAGGTGAAGGCTATGG ACACCGCCGCCGCCGCGTGCTCCGCCTACGTGTCATCCG-TTGCCGACGAGGGG ACATTGTCGGCGTCCGCGTGCTCCGGCGCTACGTGTCATCCGCTTGCCGACGAGGGG ATGGACTGTGCGCTGCGCGCTGTACGGAAAAGGTGGAGTCTTGTCACAGCTG Argeactececerceceececestarceaceasaaaserceactercreacte CGCGAGCTCAAGGCGTTCGAGGAGCAGACTCTGTTCCACTTCTACTCGGCGTCGATT ceceaecrcaaeecereerreaeeecaeacrercrerrecaerreaereearr AAGCTGGTGGACTTTGCCCATGTGGCCGAGGGTGATGGGGGTGATTGACCACAACTTCCTG AAGCTGGTGGACTTTGCCCCATGTGGCCGAGGGTGATGGGGTGATTGACCACAACTTCCTG CACGAGGTCAGCCGTCGCGCCCATAGTCCCCTTCCCCATACCATGTCCGACC GCCTCGCCAAGGACCGCGGACCACGATTCTGCTCGGATTCCGCGTCTCCGGCGTCC Gaps 63; Length 3416; 837 T; 0 U; 0 Other; IndelB Score 740.4; DB 6; Pred. No. 4.4e-145; 0; Mismatches 31;

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GCCGGGCTCTGCTCGCTGATCAAGTTCGTTTCTGACATTGTTCCGGAGACTCCTCATACG 900
                           159 TCATCGACGGCTCTGGCCTCTTCTACAAGCCGCTCCAGGCCGGCGACCGTGGGGAGCACG
                                                                             CCTTCTTCCCCCGGTTTCCACGGCACGCGACTCCTCCCCACCGAGGCGCACCCGGGGGAGC
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nutritional value; animal feed; transgenic; ds.
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CAGCCTTTGGGTCCTTCTTAAGAGGATCCTGGCA-TTTCGATTTGATAACAAAG 955
                                                      Gaps
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Pred. No. 8.4e-134;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 899 BP; 140 A; 312 C; 276 G; 171 T; 0 U; 0 Other;
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                                                                                                                                                                                                               inositol polyphosphate kinase (IPPK) DNA #5
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/product= "Maize IPPK protein #4"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rafalski JA,
                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; Page 73-74; 86pp; English.
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 643 BP; 92 A; 261 C; 178 G; 103 T; 0 U; 9 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       35.0%; Score 470.4; DB 6; Length 95.9%; Pred. No. 9.5e-89; ive 0; Mismatches 18; Indels
                                                                                                                                   Cahoon RE;
                                                                                                                                   Rafalski JA,
                                                                                                                                                                                                                                                            Claim 1; Page 74; 86pp; English.
                                                                                                         (PION-) PIONEER HI-BRED INT INC
                                                    09-JAN-2002; 2002WO-US003120
                                                                              12-JAN-2001; 2001US-0261465P
                                                                                                                                    Wang H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
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Best Local Similarity
Matches 509; Conserva
                                                                                                                                                            WPI; 2002-636540/68.
                                                                                                                                    Beach LR,
WO200259324-A2
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The invention relates to novel inositol polyphosphate kinase (IPPK) polypeptides and polynucleotides. Sequences of the invention are useful in modulating the phytic acid biosynthesis by decreasing phytate and/ or increasing non-phytate phosphorous to improve the nutritional value of animal feed, or to reduce the environmental impact of animal waste. Polynucleotides of the invention are to produce transgenic plants with an altered phenotype. IPPK proteins are used to screen compounds that modulate their activity and rahising anti-idiotypic antibodies. The present sequence is maize IPPK DNA
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                                                                                                                                                                                                                     Maize, enzyme, inositol polyphosphate kinase, IPPK, phytic acid, nutritional value, animal feed, transgenic; ds.
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89.4%; Pred. No. 8.5e-53;
tive 0; Mismatches 38;
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                                                                                                                                                                       Maize inositol polyphosphate kinase (IPPK) DNA
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519
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Best Local Similarity 89.49
Matches 328; Conservative
                                                                                                                (first entry
standard; DNA;
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The invention relates to novel inositol polyphosphate kinase (IPPK) polypeptides and polynucleotides. Sequences of the invention are useful in modulabating the phytic acid biosynthesis by decreasing phytate and/ or increasing non-phytate phosphorous to improve the nutritional value of animal feed, or to reduce the environmental impact of animal waste. Polynucleotides of the invention are to produce transgenic plants with an altered phenotype. IPPK proteins are used to screen compounds that modulate their activity and ralising anti-idiotypic antibodies. The present sequence is Eucalyptus grandis IPPK DNA
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845 GGCTCTGCTCGCTGATCAAGTTC--GTTTCTGACATTGTTCCGGAGACTCCTCATACG-C 901
                       181 AGCTCTGCTAGCTGATCAAGTTCCTTGACATTGTTCCAGANACTCCTTAGACGCC
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                                                                                                                                                                                                                                                                                                                                                               inositol polyphosphate kinase; IPPK; phytic acid; transgenic; onal value; animal feed; gene; ds.
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/product= "E. grandis IPPK protein"
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0; Mismatches 349;
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                                                                         AGCCTTTGGGTCCTTCTTAAGAGA 925
                                                                                                               AGCCTTTGGGTCCTTCCTTAAAA 264
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Local Similarity 55.6%;
les 471; Conservative
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                                                                                                                                                                                                                                                                                                                             Maize inositol polyphosphate kinase (IPPK) DNA #8
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Pred. No. 1.7e-30;
0; Mismatches 21
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                                                                           CCTCCGA 992
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nutritional val
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13.3%; Score 179;
Best Local Similarity 55.6%; Pred. No. 8
Matches 460; Conservative 0; Mismatch
/product= "Soybean IPPK
                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; Page 66-67; 86pp; English.
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                                                                                                                       09-JAN-2002; 2002WO-US003120
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nutritional value, animal feed, transgenic, gene, ds.
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                                                                                                603 GAGCGCTTGCAGAAGCTCAAGGACTGGTTCTAGACGGTGTATCACTTCTATTCT
712 GCGTCGATTCTTCTGGGCTATGATGCTGCTGCAGTCGCAGCAGCGGGAGATGGGGGTGGG
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nutritional value, animal feed; gene, ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GACATCAAGATCGGCGCCATCACGTGGCCACCGAGTTCGCCGGAGCCCTACATCGCCAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 315 GACATCAAAATCGGGTCCAGAACATGGGCGCCCAGAAGCTTCCGAGGCGTACATTGCAAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 375 TGCTTAAAAAAGGATAGGGAAAGCACAAGTATTCCATTGGGATTCAGGATCTCCGGGCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CGAGTCGTCGGCCCCGAGGGCGCCGTGGCGGACGG---AGCGCCCGGAGGTGAAGGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           435 CAAGICTATATCGATGATGGGTCAGGGTTTTATAAGCCTCATAGAAATTACATGCGTAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                538 ATGGACACCGCCGCCGCCGCGCGTGCTCCGGCGCTACGTGTCATCCGTTGCCGACGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GGAAAAGGTGGAGTCTTGTCACAGCTGCGCGAGCTCAAGGCGTGGTTCGAGGAGCAGACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GGGCCTAATGGGATATTAGCTCAACTGATGGAATTGAAGACATGGTTTGAAGATCAAACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             675 ATTTACCACTICTAGGIIGITCTITITIGIICAICTITGAAAAGAGGIIGGIGITAAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GGCGGAGATGGGGGTGGGTGACGGTGAAGCTGGTGGACTTTGCCCATGTGGCCGAGGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           735 GGT----GCTCGGTCAAACGCAGAAGTCAAACTTATTGATTTTGCTCATGTTACAGATGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TGCCTCGCCAAGGACCGCGGGACCACGAGCGTTCTGCTCGGATTCCGGGTCTCCGGCGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         495 ACCGGCCCAGCTGATGTTAGACTTCTTAGGAAATTTGTTTCTTCTAACCCGTCTGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -- GGACTGTGCGCTCGCCGCGGCGTGTACGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   555 GAGATGGAAATGCGCACAGGCCTAGGCCCGGATTGTTCTTTAGCATCTTTTGTTTATGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        694 CIGITCCACTICIACTCGGCGTCGATTCTTCTGGGCTATGATGCTGCTGCAGTCGCAGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  814 GATGGGGTGATTGACCACAACTTCCTGGCGGGCTCTGCTCGCTGATCAAGTTCGTTTCT
                                                                                                                                         Gaps
    The
                                                                                                                                                                                                                                                                                                                                                                             GAAGTAGCCTTTTATGAATCATTTTCTTCTAACAATAATATTCCAGAACACATAACG
                                                                                                                                         39;
modulate their activity and raising anti-idiotypic antibodies. present sequence is P. argentatum IPPK DNA
                                                                                                  Length 1020;
                                                           0 Other;
                                                                                                                                         Indels
                                                           'n,
                                                                                                                                         0; Mismatches 362;
                                                                                                    DB 6;
                                                           Sequence 1020 BP; 297 A; 195 C; 219 G; 309 T; 0
                                                                                                  Score 149.8; DB 6 Pred. No. 1.1e-21;
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                                                                                                                       Similarity
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9905-01139817b
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22-70N-1999;
23-70N-1999;
24-70N-1999;
26-70N-1999;
30-70N-1999;
01-70L-1999;
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23-AUG-1999;
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                                                                          Hybridisation assay, genetic mapping; gene expression control; protein identification; signal transduction pathway; metabolic pathway; promoter; termination sequence; ss.
                                                      Arabidopsis thaliana DNA fragment SEQ ID NO: 23077
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9905-0123180P

9905-0125188P

9905-0126264P

9905-0126264P

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9905-0134221P

9905-0134221P

9905-013522P

9905-0136732P

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9905-0137724P

9905-0139454P

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9905-0139455P
                                                                                                                                                                                           25-FEB-2000; 2000EP-00301439
                                 (first entry)
                                                                                                                         Arabidopsis thaliana
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05 - MAR - 1999

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16-JUN-1999;
17-JUN-1999;
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18-JUN-1999;
18-JUN-1999;
                                                                                                                                               EP1033405-A2
                               17-OCT-2000
                                                                                                                                                                     06-SEP-2000
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          AAC39023;
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CAGCCCGGGGAGCCGCATCCTCACCTCGTCCTCGACCCTCCTCGCGGGGTTTCAGGCG 348
                            395 GAAGGTTCTGATGGAGCAGCCATGATGGTGTTGGAAAATCTTCTTGCAGAATACTCAAAA 454
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                                                                                                                                         TACATCGCCAAGTGCCTCGCCAAGGACCGCGGGACCACGAGCGTTCTGCTCGGATTCCGC
                                                                                                                                                             TACATCCAAAAATGTTTGAAGAAAGACACGGGTACCACAACCGTGTCATCGGGTTTCAGG
                                                                                                                                                                                                            GTCTCCGGCGTCCGAGTCGTCGCCCCCGAGGCCCC---GTGTGGCGGACGGAGCGCCCG
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                                                                                                                                                                                                                                         575 ATCTCTGGTTTCGAAGTGTATGATCACAAGAATCGAGTTTCTGGAAGCCCGAGAGGAAG
                                                                                                                                                                                                                                                                            526 GAGGTGAAGGCCATGGACACCGCCGGCGTCCGCCGCGTGTCCGCCGCCTACGTGTCA---
                                                                                                                                                                                                                                                                                                             CTTCTTCGCGGGCTCGATGTAGATGGAGGATTGACTCTGAGGAAGTTTGTATCATCT
                                                                                                                                                                                                                                                                                                                                                                                                                GGAAAAGGTGGAGTCTTGTCACAGCTGCGCGAGCTCAAGGCGTGGTTCGAGGAGCAGACT
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                                                                      CCCTGCGTCGCAGACATCAAGATCGGCGCCATCACGTGGCCACCGAGTTCGCCGGAGCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Arabidopsis thaliana DNA fragment SEQ ID NO: 3949.
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99US-0123180P.
99US-0123548P.
99US-0125788P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAC33685 standard; DNA; 1104
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05-MAR-1999;
09-MAR-1999;
23-MAR-1999;
25-MAR-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAGCTGGGCCCCCTCATCGACGGCTCCGGCCTCTTCTACAAGCCGCTCCAGGCCGGCGGCTC 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cacarcc --- aragararrrcccegnerarcaceecacrcaa------ecaerr 394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAGCCTGGTCCTCTCGTAGATGACAAGGGTCGGTTCTTCAAGCCACTTCAGGGCGATTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                <u> aacaagargcagcrcaaagrcccrcaacarcagcrrcaagacacacarrccraaagaccag</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CGTGGGGAGCACGAGGTCGCCTTCTATGAGGCGTTCTCCGCCCACGCCGCCGTCCCGGCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 148.6; DB 3; Length
Pred. No. 2e-21;
0; Mismatches 369; Indels
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9905-0151080P.
9905-0151303P.
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9905-0151310P.
9905-0153070P.
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99US-0155486P

99US-0155659P

99US-0156596P

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99US-0159294P
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99US-0160815P.
99US-0160980P.
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99US-0161406P.
99US-0161360P.
99US-0161361P.
99US-0161920P.
99US-0161920P.
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99US-0160989P
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99US-0162142P
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Best Local Similarity 53.0%;
Matches 453; Conservative
 26-AUG-1999;
27-AUG-1999;
27-AUG-1999;
30-AUG-1999;
31-AUG-1999;
01-SEP-1999;
07-SEP-1999;
10-SEP-1999;
113-SEP-1999;
115-SEP-1999;
15-SEP-1999;
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Hybridisation assay; genetic mapping; gene expression control; protein identification; signal transduction pathway; metabolic pathway;
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23-MAR-1999;
25-MAR-1999;
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04-MAY-1999;
05-MAY-1999;
06-MAY-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CACATCC---ATAGATATTTCCCGGTGTATCACGGCACTCAA------GCAGTT 344
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10.9%; Score 147; DB 3; Length 1243;
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Matches 452; Conservative 0; Mismatches 370; Indels 3
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Search completed: June 16, 2005, 22:53:21 Job time: 794 secs